09/613/186

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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 36, Applisequence 36, Applisequence 36, Applisequence 36, Applisequence 4, 
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                                                                                                                                                                                             7, 2003, 14:47:43; Search time 21 Seconds (without alignments) 398.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                   US-09-613-486-15
991
1 MELMSDSNLSNLVITDASSL......GGVVNTPVSNLRQLGRREVM 198
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-10-51B-2
US-09-10-51B-2
US-08-135-2
US-08-770-544-16
US-09-770-544-16
US-09-79-252-91A-32657
US-09-252-991A-32657
US-09-252-991A-32657
US-09-252-991A-32657
US-09-252-991A-32657
US-09-381-13
US-09-484-105-16
US-08-484-105-16
US-08-484-105-16
US-08-484-105-16
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US-09-252-991A-31879
US-09-252-991A-21752
US-09-171-699-10
US-09-171-548C-46
US-09-328-352-7238
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-09-107-532A-6952
-09-252-991A-17176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328717 seqs, 423:0858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/l.
2: /cgn2_6/ptodata/l.
3: /cgn2_6/ptodata/l.
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Match Length
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73.5
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No.
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24, Appl 26, Appl: 5, Appl: 13, Appl: 18, Appl: 11, Appl: 11, Appl: 11, Appl: 11, Appl: 2, Appl: 2, Appl: 2, Appl: 2, Appl: 10, Appl: 10, Appl: 10, Appl: 10, Appl:			
Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 4 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 2 Sequence 3 Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 3		PROTEINS	(
69.5 7.0 1713 3 US-08-600-982-24 69.5 7.0 1713 5 US-08-600-982-24 69.5 7.0 2042 4 US-09-07-0594-24 69.5 7.0 2042 4 US-09-07-0594-6 69.5 7.0 2285 4 US-09-308-375-2 68.5 6.9 389 4 US-09-328-322-6865 68.6 6.9 693 1 US-08-24-917-11 68.6 6.9 693 2 US-08-24-917-11 68.6 6.9 693 5 PCT-US95-0393-4A-1 68.6 6.9 893 5 US-08-24-917-11 68.6 6.9 893 5 US-08-24-917-11 68.6 6.9 893 5 US-09-368-5-5 67.5 6.8 875 1 US-09-368-5-477 67.5 6.8 875 3 US-08-463-949A-10	ALIGNYENTS	### 15. Application US/39080983 **o. 6.97948 **invermation**: Canit: dial-Ying **CANT: Ling, Kai-Ying **CANT: Ling, Kai-Ying **CANT: Ling, Kai-Shu **CANT: Gonsalves, Dennis **BERTINON: And THEIR USES **BR OF SEQUENCES: 23 **SPRONDENCE ADRESS: **RECES: Nixon, Hargrave, Devans & Doyle LLP **RECES: Nixon, Hargrave, Devans & Doyle LLP **RECES: Nixon, Hargrave, Devans & Doyle LLP **RECES: Nixon, Hargrave, P.C. Box 1051 **TER READABLE FORM: **TER READABLE FORM: **THE TAILON NUMBER: US 60/047,194 **THE GOLD NUMBER: US 60/047,194 **THE MARKET STATION **THE GOLD NUMBER: US 60/047,194 **THE GOLD NUMBER: US 60/047,194	1 Similarity 100.0%; Pred. No. 1.7e-105;
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Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR APPLICATION NUMBER: US 60/074,190
RAIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF ES QID NOS: 33142
SEQ ID NO 30374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 EFLNEFNLICRENNLIINDNKTKVDNFPFVDKSSKSDIFSFFENITSTN'SNDKWIKEISN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 FIDYCVNEEHLGNKGAIKCIFPVI-----TNTLKQKKVDTKNI-DNIFSKRNNYTNFN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ----NELIKVTKADAPAFYQGILELKGQLRRLETLGKPVVAAINGAALGGGWEICLACHH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 NSFGERNVVVTEGDLKKVIDGCAPLIRFINKLRIFGRTFIEAY------VDFCIAYKH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ASSLNGVDK--KLLSA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 EVERMINOKGAPNEG-IEVVFGLILYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 ANTHNGVYREAMAKTIARLEAEK----EGIA---GVVL-----TSAKKTFFAGGDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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8.2%; Score 8.1; DB 4; Length 732;
Best Local Similarity 22.4%; Pred. No. 1.9;
Matches 30; Conservative 26; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.6%; Score 85; DB 2; Length 599; Best Local Similarity 24.3%; Pred. No. 0.5; Matches 36; Conservative 26; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 DLKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 VFEKILDLSLKDSRLTNKFLTFFENINE 400
                                                                                                                                                                                                                                                                                                      NAME/KEY: phage abortive infection LCCATION: N/A IDENTIFICATION METHOD: based upon DNA OTHER INFORMATION: phage resistance OTHER INFORMATION: enzyme AbiE PUBLICATION INFORMATION: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ELMSDSNL----SNLVITD-
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                                                  HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: Bacterium
CELL LINE: N/A
ORGANEILE: N/A
IMMEDIATE SOURCE:
LIBRARY: Genomic
CLONE: SMQ-20
                                                                                                                                                                                                                                          POSITION IN GENOME: N/A FEATURE:
                                  DEVELOPMENTAL STAGE:
  INDIVIDUAL ISCLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-252-991A-30074
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                                                                                                    61 IISPKVQRADSOVIFSNSFGBRNVVVTBGDLKKVLDGCAPLTRFINKLRTFGRTFIEBYV 126
                                                                                                                                   DFCIAYGHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQOSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                                  1 MELMSDSNISNLVITDASSINGVOKKILSAEVEKMIVQKGAFNEGIEVVFGLLLYALAAR 60
                            APPLICANT: Sivain Moineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenbergh,
APPLICANT: Benezer R. Vedamuthu, Jeffrey K.
APPLICANT: Benezer R. Vedamuthu, Jeffrey K.
APPLICANT: Benezer R. Vedamuthu, Jeffrey K.
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: lactis, and Method of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version: 4)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/910,551B
FILING DATE: August 11, 1997
CLASSIFICATION: 435
RICH APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTOREY/AGENT INFORMATION:
NAME: Ian C. McLead
REGISTRATION NUMBER: 20,93:
RELECOMMUNICATION INFORMATION:
TELECHONE: (5.7),347.4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 48664
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08910551B
Patent No. 5910571
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: No FRAGMENT TYPE: N/A ORIGINAL SOURCE: ORIGINAL SOURCE: STRAIN:
                                                                                                                                                                                                                                                                                                                                 181 VVNTPVSNLRÇLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (517) 347-4103
TELEX: No. 5910571e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ian C. McLeod
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MOLECULE TYPE:
DESCRIPTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-910-551B-2
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FILING DATE:
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Quaranta, Vito
APPLICANT: Hormia, Marketta
APPLICANT: Hormia, Marketta
TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion
TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 RITSPKVQRADSDVIFSNSFGERNVV-VTEGDLKKVLDGCAPLTRFINKLRT-FGRT--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 ELLNEAKMTRKRLQÇEINPALNSLQQTLKTVSVQKDLLDAN------VTAV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 RNDLRGIQRGDIDSVVS----GAKSMVRKANGITSEVLDGSAPSRRIWEGLRTATGCTRHE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ELMSDSNLSNLVITDA--SSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 79.5; DB 1; Length 770; 26.6%; Pred. No. 3.1; tive 22; Mismatches 54; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PIOR APPLICATION DATA:
APPLICATION NUMBER: US C8/151,134
FILING DATE: 12.NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: DESXOS.002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : | : | 449
| DFNKALIDANNSVKKLTKKJPDL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 -FTEAYVDFCIAYK---HKLPQL 133
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US-08-770-544-16
; Sequence 16, Application US/08770544
                                                                                                         Sequence 2, Application US/08445135
Patent No. 5658789
  144 RIALDNPGVQLGLP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.6%
Marches 38; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: I
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                                                                                       US-08-445-135-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DFCIAYKHKLPQLNAAAELGIP------AEDSYLAADFLGTCPKLSELQQSRKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 DGYRVETEL-----GQKRVYLSYSEVREAILGGKYGASP----TNTVRSFWRYFAHTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: Sonsalves, Dennis
APPLICANT: Sonsalves, Mai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
8.0%; Score 79; DB 2; Length 477;
Best Local Similarity 21.0%; Pred. No. 1.8;
Matches 43; Conservative 40; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
                                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle Lip
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
CTATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gonsalves, Dennis
Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06 0009008
FILING DATE: 21-DEC-1955
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael 1.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 FASMYALKTEGGWWNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 MACAIAIKS ------ANLRRKG 467
                                                                                                                                                                                                                            CITY: Rochester STATE: New York COUNTRY: Us.A. ZIP: 14603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09579259
Patent No. 6558953
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NC: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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518 LEGDAQLS--AVASLYGLKLDG-----IDGEQALGR 546
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                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                 7 SNISNLVITDASSLNG-VDKKLLSAEVEKMLVQK---
                                                                                                                                                          Query Match 7.8%; Score 77.5; D
Best Local Similarity 25.0%; Pred. No. 2.1;
Matches 60; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                           LENGTH: 410
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-32657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 33; Conserv
                                                                                                      US-09-252-991A-20306
9080Z ON GI ČES
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US-C9-080-983-13
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.118
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 LPITEALQIN-----ARLRRLVLSKGGSQTPRDMGNMIVAMIQLFVLYSTVKNISVK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 DGYRVETEL-----GGKRVYLSYSEVREAILGGKYGASP----TNTVRSFMRYFAHTTI 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSPKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.0%; Score 79; DB 4; Length 477;
Best Local Similarity 21.0%; Pred. No. 1.8;
Matches 43; Conservative 40; Mismatches 60; Indels
                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1SM PC compatible
OPENTING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/579,259
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKST NUMBER: 1963/621
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 6009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-579-259-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 FASMYALKTEGGVVNTPVSNLRQLG 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                 STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-20306
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US-09-252-991A-32657

| Sequence 32657, Application US/0925291A
| Sequence 32657, Application US/0925291A
| Sequence 32657, Application US/0925291A
| Setural 32657, Application US/0925291A
| TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TILE REPERRINCE: 107196.136
| TILE REPERRINCE: 107196.136
| CURRENT APPLICATION NUMBER: US/09/252,991A
| CURRENT FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| EDGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                        97 -----GCAPLTRFTNKLRT-----FGRTFTEAYVDFCIAYKHKLPQLNAAAELGIP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 APLTRFTNKLRTFGRTFTEAYVDFC-LAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AALFRGTELLHPSGSTILEADDILCVIGHEHDLP---ALGKLFSQAPDRGLGARFFGDFV 517
                                                                                                                                                                                                      78 SGMDGLAFLRHASLSGKVHSVILSSEVDPILRQATISMIECLGLNFLGJLGKP-FSLERI 136
                                                                                                                                                                                                                                                                                                                                                    137 TALLTRYNARRODLPROIEVAELPSVADVVRGLDNGEFEAYYOPKVALDGGGLIGAEVLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 VHPSQLGSRALAENISALLTEFHLPPSSVMFE1----TFTGLISAPASSLENLVRLRIM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 RWNHPHLGVLPPSHFLYVMETYNLVOKLFWQLFSQG-----LATRRKLAQLGQPINLAFN
                                                                                                                                          - -GAPNEGIEVV
                                                                                                                                                                                                                                                                                 50 FGLLLYALAARTTSPK-VGRAD----SDVIFSNSFGE-----RNVVVTEGDL--KKVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AEDSYLAADFL--GTCPKLSE--LQQSRKMFASMYALKTEGGVVNTPVSNLRQLGRREVM
                                                                   59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09080983
Parent No. 6197948
SENERAL INFORMATION:
APPLICANT: Zhu, Hai-Ying
APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
APPLICANT: Gonsalves, Demis
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS TYPE 2 PROTEINS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.8%; Score 77; DB 4; Length 597; ilarity 34.0%; Pred. No. 4.1; Conservative 8; Mismatches 44; Indels
                                                                       Indels
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328 -----YTINYIDFGWXGHLSAGLRQKLTQ----AVLALYTKDAYRIEKAVLRLC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 MEEMSGKNINHIMMAENKTETFITGIQNKQLKQEVAKLIVE----NFMKQVFDDGFFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ----GLLLYALAARTTSPKVQRADSDVIFSNSFGE---RNVVVTEGDLKKVLDGCAPLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 FINKLRIFGRIFTEAYVDF-----CLAYKHKIPQLNAAAELGIPAEDSY-LAADFLGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : MELMSDSNLSNLVITDASS----LNGVDKKLLSAEVEKMLVQKGAPNEGIEVVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.5%; Score 74.5; DB 4; Length 587; Best Local Similarity 22.6%; Pred. No. 7.8; Matches 43; Conservative 27; Mismatches 65; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: 11, Joachim J
APPLICANT: 11, Joachim J
TITLE ORVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 DPHPGNLLFHVLTKEEGTGASR-KTETVHEKEFGSFAFRASTSAE
                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/055,598
FILING DATE: 13 May 1998
APPLICATION NUMBER: 60/05571
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
; LCCATION: (B) LOCATION 1...587
; SEQUENCE DESCRIPTION: SEQ ID NO: 6405:
US-09-107-532A-6405
                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
       MEDIUM TYPE: CD/ROM ISO9660
                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-507
TELEPAK: (781)893-8277
INFORMATION FOR SEQ ID NO: 6405:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: S87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16, Application US/08484105; Patent No. 5589341; GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RINE, Jasper
POSS, Margit
MCNALLY, Francis J
LAURENSON, Patricia
HERSKOWITZ, Ira
LI, Joachim J
GAVIN, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STILLMAN, Bruce
BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 PKLSELQQSR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 QQEGSFDESR 382
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APPLICANT;
APPLICANT;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TISPKVQRADSDVIESNSFGERNVVVTEGJIKKVLDG-----CAPII----RFTNKLRTFG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 SISEKVKYVGS-----HTYVVDGKTYTVLDAWVFNYMKSLTKKYKRVNGLRAFC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 RTFTEAYVDFCIAYKHKLPQLMAAAELGIPAEDSYLAADF1-GTCFKLSELQGSRKMFAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 CACEDLYLTVAPIMSERF-KTKAVGMKGLPVGKEYLGADFLSGTSKLMSDHDRAVSIVAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 LKNENYSSV---DSSRLSDSEVKEVLEKSKESFKSELASTDE--HFVYHIFFLIRCAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MSDSNLSNLVITDASSLNGVD-KKLLSAEVERMILVQKGAPNEGIEVVFGLLLYAL--AAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.7%; Score 76; DB 3; Length 223; 23.3%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEB: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/C80,983
                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERSONE/DOCKET NUMBER: 19603/1631
TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1500
INFORMATION FOR SEC ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 MYALKTE- -- GGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: :| |||
199 KNAVDRSAFTGG--ERKIVSLYDLGR 222
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAX-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6405, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 223 amino acids amino acids
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Best Local Similarity 23.34
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS
                                                                                       STATE: New York COUNTRY: U.S.A. ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-6405
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SOFTWARE: Microsoft Office 97
SEQ ID NO 36
LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 706 amino acids
amino acid
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MOLECULE TYPE: protein
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                    California
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 SRLIVVAVANTMDLPERILSNRISSRLGLSRVPFEPYTHTQLEII------IÄÄRLEAV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 SNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNE-----GIEVVFGLLLYALAARTTSP 64
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APPLICANT: BELL, Stephen P
APPLICANT: KOBAYSHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: HERSKOHITZ, Ira
APPLICANT: LATENSON, Patricia
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOUDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.4%; Score 73.5; DB 1; Length 706; Best Local Similarity 19.3%; Pred. No. 13; Matches 43; Conservative 33; Mismatches 68; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GIPAEDSYLAADFLGTCPKLSELQQSRKMFASXYALKTEGGVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645 ---AE-----AKFGELILRRPEFGYVLSSLSENGVL 672
FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                        ZIP: 94111-418/
COMPUTER REDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: BC-BOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: BC-BOS/MS-DOS
ATTORNEY/AGNT: INFORMATION:
FILING DATE: TASAITION NUMBER: 36,627
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
RELEASA: (415) 494-870
TELEFAX: (415) 494-871
SEQUENCE CHARACTERISTICS:
JENGTH: 706 arino acids
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             STREET: 4 Embarcadero Center, Suite 3403
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08484106
Patent No. 5614618
GENERAL INFORMATION:
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; MOLECULE TYPE: protein
US-C8-484-105-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                   COUNTRY: USA
ZIP: 94111-4187
ADDRESSEE:
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532 R----DDDVFSSDAIRFAARKVAAVSGDARRALDICRRASELAENKNGKVTPGLIHQAIS 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match
7.4%; Score 73.5; DB 1; Length 7
Best Local Similarity 19.3%; Pred. No. 13;
Matches 43; Conservative 33; Mismatches 68; Indels
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Fanduy, 1200 O.
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trnA Synthetase;
FILE REFERENCE: BE-1193
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 66/093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 31
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

XEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFUTER: IBM PC compatible
CONFIDENT SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PatentIN Release #1.5, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/484,106
FLING DATE:
CLASSIFICATION NUMBER: US/C8/484,106
FLING CASSIFICATION NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERX: (415) 494-8771
TELEFERX: (415) 494-8771
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; ORGANISM: Saccharomyces cerevisiae
US-09-357-251-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-357-251-36
; Sequence 36, Application US/09357251
; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
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PRIOR APPLICATION DATA:

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                                                                                                                         134 LTDETQSILAQIKNNSHLDSIDAKILNDLKKRKLJAQGKITDFSVTKGPE--FSTDLTKL 191
                                                                                                                                                                                  58 AARTTSPKVQ-RADSDVIFS-NSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRT--FGR 113
                                                                                                                                                                                                                                                                          114 TFTE----AYVD-----FCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELCQ 164
                                                                                                                                                                                                                                                                                                     245 GFTEMPSNQYVETGFMNFDALY---VPQQHPARDL----QDTFYIKD-----PLTAELFD 292
                                                                                                                                                                                                                           192 ETJIJSDAVSTNAYKDLKFKPYNFNSQGVQISSGALH------PLNKVREEFRQIFFSM 244
                                                                                            4 MSDSNLSNLV-ITDASSLNGVDKKLLSAEVEKMLVQKG-----APNEGIEVVFGLLYAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 FGEWTEVVID-DILPTINGDIVFS-FSTSMNEFWNALLEKAYAKLLGCYE-----A
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                                                  Gaps
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                                                  40;
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; Patent No. 5310678
APPLICANT: Bingham, Richard W.; Chambers, Philip; Emmerson, Title OF Invention: NEWLS CORS. 3
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATE: 17-NOV-1989
; FILING DATE: 17-NOV-1989
       OB 3; Length 503;
                                             74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 2 DIABETES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: POLONSKY, KENNETH S.
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: COX, NACHISA
APPLICANT: COX, NACHISA
APPLICANT: COX, NACH'SA
APPLICANT: CX, NACH'SA
APPLICANT: ZHOU, VIN-PING
APPLICANT: ZHOU, VIN-PING
APPLICANT: ZHOU, VIN-PING
APPLICANT: AND IN CENICH
APPLICANT: HANIS, CRAIG I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENITON: XETHONS OF TREATMENT OF TYP
FILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/C9/422,969
CURRENT FILING DATE: 1999-10-21
ERRLIER FILING DATE: 1999-05-13
NUMBER OF SEC ID NOS: 30
ch 7.4%; Score 73; DB 3
I Similarity 24.6%; Pred. No. 9.2;
48; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/09422869
Patent No. 6235481
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SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-C9-422-869-26
  Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6235481
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-422-869-26
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347 CTRIVTPFM----SPQIYSCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCV 402
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                                                                                                                                                                                                                                                                                 289 LPSVGNLNNMRATYLETLSVSTTRGFASALVPKVVTQVGSVIBELDTSYCIETDLDLY-- 346
                                                                                                                                                                                                                                                                                                                                   58 AARTISPKVQRADSDVIPSNSFGERNVVV---TEGDLK------KVLDGCAPLT-RFT 105
                                                                                                                                                                                                                                         3 LMSDSNLSNLVITDASSLN-GVJKKLLSAEVEKMLVÇKGAPNEGIEVVF----GLLLYAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                   106 NKLRTFGRIFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQS
                                                                                                                                                                                       32; Gaps
                                                                                                                                          Query Match 7.3%; Score 72; DB 6; Length 553; Best Local Similarity 24.1%; Pred. No. 14; Matches 49; Conservative 28; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: November 7, 2003, 14:50:55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 QVIITGNLDISTELGNVNNSISN 476
APPLICATION NUMBER: 885,765
FILLING DATE: 15-JUL-1986
ID NO:1:
                                                                        LENGTH: 553
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Conservative
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  69
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Apply Sequence 2, Apply Sequence 3,074, A Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 13, Appl Sequence 13, Appl Sequence 16, Appl Sequence 16, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 11752, A Sequence 1752, A Sequence 1752, A Sequence 1752, A Sequence 4, Appl Sequence 4, Appli Sequence 6, App
                                                                                                                                             7, 2003, 14:47:43; Search time 2: Seconds (without alignments) 398.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                              US-09-613-486-15
991
1 MELMSDSNLSNLVITDASSL.......GGVVNTPVSNLRQLGRREVM 198
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    /cgn2 6/ptodata1/liaa/5A_COMB.pep:*
    /cgn2 6/ptodata1/liaa/5B_COMB.pep:*
    /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
    /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
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    /cgn2 6/ptodata1/liaa/PcTUS_COMB.pep:*
    /cgn2 6/ptodata1/liaa/PcTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-910-511B-2
US-08-45-135-2
US-08-445-135-2
US-08-770-544-16
US-09-252-991A-32657
US-09-252-991A-32657
US-09-252-991A-32657
US-09-107-532A-6405
US-09-367-251-36
US-09-37-251-36
US-09-252-991A-31879
US-09-383-37-38
US-09-38-38-37-38
US-09-38-38-37-38
US-09-38-38-37-38
US-08-671-5480-4
US-08-972-38-38-37-6918
US-09-107-532A-6952
US-09-252-991A-17176
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                                                                                                                                                                                                                                                                                                                                                                                     328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Match Length DB
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70.5
70.5
69.5
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Sequence:
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Maximum DB e
                                                                                                      OM protein
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-600-982-24 Sequence -694-10261A-24 Sequence -304-10261A-24 Sequence -304-512A-4807 Sequence -984-618-13 Sequence -107-522A-4807 Sequence -124-917-11 Sequence -124-917-11 Sequence -124-917-11 Sequence -136-647A-5 Sequence -136-985-2 Sequence -136-985-2 Sequence -136-985-2 Sequence -136-985-2 Sequence -136-985-2 Sequence -136-985-2 Sequence -146-985-2 Sequence -146-985-3 Sequence -146	ô
-600-982-24 -694-10261A-24 -10368-24 -1038-375-26 -194-618-13 -107-522-6865 -463-620-11 -1228-352-6865 -463-620-11 -1238-352-4377 -136-620-11 -1356-393-11 -1358-393-11 -1358-393-11 -1358-393-11 -1358-393-11 -1358-393-11 -136-201	Saps
-600-982-24 -894-10261A-24 -307-0984-6 -3084-618-13 -984-618-13 -984-618-13 -107-532A-4807 -1453-620-11 -924-853-11 -924-853-11 -924-853-11 -925-932-11 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-985-2 -926-983-2 -983-	1398
69.5 7.0 1713 3 69.5 7.0 1713 5 69.5 7.0 1713 5 69.5 7.0 2042 4 69.5 7.0 2042 4 69.5 7.0 2042 4 66.5 6.9 7.0 363 3 68.5 6.9 382 4 68.5 6.9 382 4 68.5 6.9 382 4 68.5 6.9 693 2	RECERRING NORTHERN: 30,727 REFERENCE/DOCKET NUMBER: 19603/1631 TELEPHONE (106) 263-1304 TELEPHONE: (116) 263-1304 TELEPAX: (116) 263-1304 INFORMATION FOR SEQ ID NO: 15: SECUENCE CHARACTERISTICS: LENGTH: 198 amino acids TYEE: amino acids TYPE: amino acids STRANDENESS: TOPOLOGY: linear MOLECULE TYPE: protein S.09-080-983-15 Query Match Best Local Similarity 100.0%; Pred. No: 1.7e-105; Matches 198; Conservative 0; Mismatches 0;

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMING ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE:
107196.136
CURRENT PEPEIGATION:
PRIOR ENPLICATION NUMBER: US,09/252,99.A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF EQ. ID NOS: 33.42
SEQ ID NO 3.074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 FIDYCVNEEHLGNKGAIKCIFPVI-----TWILKQKKVVDTKNI-DNIFSKRNMVTNFN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 NSFGERNVVTTEGDLKKVIDGCAPITRFTNKLRTFGRTFTEAY------VJFCIAYKH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 ----NELIKVTKADAPAFYQGILELKGQLRRLETLGKPVVAAINGAALGGGWEICLACHH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 BFLNEFNLICRENNLIINDNKTKVDNFPFVDKSSKSDIFSFFENITSTNSNDKWIKEISN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- ASSLNGVDK--KLLSA 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 ASSINGVDKKLLSAEVEXMIJVQKGAPNEGIEVVFGLLIYALAARTISPKVQRADSJVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 ANTWAGVYREAMAKTIARLEAEK-----GIA---GVVZ------TSAKKTFFAGGDJ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 EVEKMINQKGAPNEG-IEVVFGILLYALAARTTSPKVÇRADSDVIFSNSFGERNVVVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.2%; Score 81; 3B 4; Length 732;
Best Local Similarity 22.4%; Pred. No. 1.9;
Matches 30; Conservative 26; Mismatches 50; Indels 28; Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.6%; Score 85; DB 2; Length 599;
24.3%; Pred. No. 0.5;
vative 26; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 DIKKVLDGCAPLIRFTNKLRTFGRIFTE 117
                                                                                                                                                                                                                                                                                                            LOCATION: N/A

LOCATION: N/A

LOCATION: N/A

LOCATION METHOD: based upon DNA

OTHER INFORMATION: phage resistance
OTHER INFORMATION: enzyme Abis

PUBLICATION INFORMATION: N/A

US-08-910-551B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 VFEKILDLSLKDSRLTNKFLTFFENINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30074, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                          NAME/KEY: phage abortive infection incoming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ELMSDSNL----SNLVITC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 KIPCINAAAELGIF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%
Best Local Similarity 24.3%,
Matches 36; Conservative
INDIVIDUAL ISCLATE: WI
DEVELOPRENTAL STAGE: N
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CELL LINE: N/A
ORGANELLE: N/A
                                                                                                                                                                                   CLCNE: SMQ-20
POSITION IN GENOME: N
                                                                                                                                                                    LIBRARY: genomicional CLCNE: SMQ-20
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US-09-252-991A-30074
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                                                                                                                             61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                             DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                       MELMSDSNLSNLVITDASSLNGVDKKLLSAEVERMLVQKGAPNEGIEVVFGLLLYALAAR 60
                                 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR 60
                                                                                                 TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Encoding Phage
Aborive Infection Protein
From Lactococus
lactis, and Method of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sylvain Moineau, Barbara APPLICANT: Sylvain Moineau, Barbara APPLICANT: Sylvain Moineau, Barbara APPLICANT: J. Holler, Peter A. Vandembergh, APPLICANT: Kondo Defer S. Vedamuthu, Jeffrey K. APPLICANT: Kondo Defer S. Vedamuthur. Selfing Phage TITLE OF INVENTION: Abortive Infection Protein TITLE OF INVENTION: From Lactococcus TITLE OF INVENTION: lactis, and Method of Use NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,551B
FILING DATE: August 11, 1997
CLASSTEICATION A43
PRICHATON NUMBER: US/68,907
FILING DATE: December 1, 1995
ATOMENSY/AGENT INFORMATION:
ATOMES APPLICATION NUMBER: 20,931
REGISTRATION NUMBER: (20,931
RELEPRANCE (517) 347-4103
TELEFAX: (527) 347-4103
TELEFAX: (527) 347-4103
TELEFAX: (527) 347-4103
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS (version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Dissette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
COMPUTER: Acer
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08910551B Patent No. 5910571
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                                                                                                                                                                                                                                                                                          181 VVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2: Ian C. McLeod
2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                   181 VVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: Protein POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: N/A ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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STREET: 21
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US-08-910-551B-2
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Gaps

Sequence 26, App. Sequence 13, Appl Sequence 733, Appl Sequence 10, Appl Sequence 5013, Appl Sequence 5013, Appl Sequence 10878, Appl S

App.

Sequence 16, Appl.
Sequence 18, Appl.
Sequence 5570, Ap
Sequence 5570, Ap
Sequence 13, Appl.
Sequence 113, Appl.
Sequence 1, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 3, Appl.
Sequence 666, Ap
Sequence 160, Appl.
Sequence 17, Appl.
Sequence 1805, Ap
Sequence 1805, Appl.
Sequence 1804, Ap

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Sequence 36, Appl
Sequence 10721, A
Sequence 10, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 1788, A
Sequence 177, Appl
Sequence 1885, Ap
                                                                                                    7, 2003, 14:49:54; Search time 23 Seconds (without alignments) 1172.633 Million cell updates/sec
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                                                                                                                                                                         US-09-613-486-15
991
1 MELMSDSNLSNLVITDASSE.....GGVVNTPVSNLRGLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

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| cgn2_6/ptodata/2/pubpaa/PCT_RBM_PUBLEPpp:*
| cgn2_6/ptodata/2/pubpaa/PCT_RBM_PUBLEPpp:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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12 US-10-138-842A-37

9 US-09-115-242-10721

12 US-10-138-842A-16

12 US-10-039-112-16

13 US-10-032-585-7808

14 US-10-156-76-11789

15 US-10-156-76-11789

15 US-10-156-76-1289

15 US-10-25-301-1385

15 US-10-25-301-1385

15 US-10-25-301-1385

16 US-10-156-76-12518

17 US-10-156-76-12518

18 US-10-156-76-12518

19 US-10-186-76-12518

19 US-10-186-76-12518
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      644079 segs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                      OM protein - protein search, using
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length: 200000000
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Match Length DB
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223
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Maximum DB seq
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ALIGNMENTS

68.

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QRADSDVIFSNSF-GERNVVVTGGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
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28.9%; Score 286; DB 12; Length 264; 37.6%; Pred. No. 1.8e-24; ive 29; Mismatches 87; Indels ;
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Beet Yellow Virus
                                                                                                                                                                                                                                          71; Conservative
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Best Local Similarity
Matches 71; Conserv
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71 NVQPISTFIKASFGGGKELYJTHGELNSFLGSQKLLEGKPNKLRCFCRTFQKDYISLRKE 130
                                        126 YKHKLPQUNAAAELGIPAEDSYLAADFIGTCPKLSELQQSRKMFASMYALKTEGGVVNTP 185
                                                                                131 YRGKLPPIARANRHGLPAEDHYLAADFISTSTELTDLQQSRLLLARENATHTEFS-SESP 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LVITDASSLNGVDKKLLSAEVERMLVQKG----APNEGIEVVFGLLLYALAARTIS---- 63
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                                                                                                                                                                                                                                                           PUDICATION NO. US20030148395A;
PUDICATION NO. US20030148395A;
PUDICATION NO. US20030148395A;
PUDICANT: GONSALVES, DENNIS
APPLICANT: LING, KAI-SHU
APPLICANT: LING, KAI-SHU
APPLICANT: LING, KAI-SHU
TITLE OF INVENTION: THERE USES
FILE REFERENCE: 07678/02506
TITLE OF INVENTION: THERE USES
FILE REFERENCE: 07678/02506
CURRENT APPLICATION NUMBER: US 09/579,259
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR APPLICATION NUMBER: US 09/579,269
PRIOR FILING DATE: 1998-12-31
NUMBER: OF SEQ ID NOS: 67
SCF ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
12.2%; Score 120.5; DB 12; Length
Best Local Similarity 25.8%; Pred. No. 2e-05;
Matches 54; Conservative 31; Mismatches 69; Indels
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Sequence 10721, Application US/09815242

; Patent No. US2002061569A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ohlsen, Kari L.
Zyskind, Udúth W.
Zyskind, Udúth W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Citrus Tristeza Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari J.
                                                                                                                            186 VSNLRQLGR 194
                                                                                                                                                                190 VTSLKOLGR 198
                                                                                                                                                                                                                                                    JS-10-138-842A-37
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APPLICANT:
APPLICANT:
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APPLICANT:
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96 DGCAPLTRFTN--KLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADF1 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 OKEALYALA----SEEVPSQDSEEKVIVIATRNPGKAKEFSSIFGEKGYTV-----KTILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MELMSDSNLS---NLVITDASSL-----NGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 Application US/10138842A
Sublication No. US20030148390A1
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
APPLICANT: GONSALVES, DENNIS
TILLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND TILLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND TILLE OF INVENTION: THEIR USES
FILE REPERENCE: 07678 602506
CURRENT APPLICATION NUMBER: US 010,203
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR PLING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 08/770,544
PRIOR PRILING DATE: 1998-12-31
PRIOR PLING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 67
SUPPLIED AND SEC TO WINDOWS VERSION 4.C
SEQ ID NO 16
LENGTH: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

8.0%; Score 79; DB 9; Length 451;
Best Local Similarity 24.2%; Pred. No. 3.2;
Matches 53; Conservative 27; Mismatches 73; Indels
IIIJE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GTCPKLSELQQSRKMFASMYALKTEGGVVNTPVSNLRQL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GIYSARFAGEPTNDASNNAKLL 356
                                                        TYPE: PRT CRGANISM: Enterococcus faecalis US-09-815-242-10721
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12;

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IVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSPKVQ
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19.6%; Pred. Nc. 10;
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                                                                                                                                                                                                                                                                       169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                             452 MACAIAIKS-----ANLRRKG 467
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7808, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (403)...(403)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                   121 DFCIAYKHKLPQLNAAAELGIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGVVNTPVSNLRQLGRREV 197
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CRGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (403)..(403)
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Best Local Similarity
Transes 39; Conserva
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                                                                                                                                                                                                                          ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                      354 DGYRVETEL-----GQKRVYLSYSEVREAILGGKYGASP----TNTVRSFMRYFAHTTI 403
                                                                                                                                                                                 332 IPITEALQIN-----ARLRRLVLSKGGSQTPRDMGNMIVAMIQLFVLYSTVKKISVK 353
                                                                                                                                                                                                                                                                                                           121 DFCIAYKHKLPQLNAAAELGIP-----AEDSYLAADFLGTCPKLSELQQSRKM 168
                                                                                                                                                                                                                                                                                                                                                      --- KANA 451
                                                                                                                                           12 LVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSFKVQ 67
                                                                                                        Gaps
                                                                                                      62:
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8.0%; Score 79; DB 12; Length 477;
Best Local Similarity 21.0%; Pred. No. 3.5;
Matches 43; Conservative 40; Mismatches 60; Indels
                                                                Length 477;
                                                                                                                                                                                                                                                                                                                                                  404 TLLIEKKIO-PACTALAKHGVPKRFTPYCFDFALLDNRYYPADVL----
                                                         ; Score 79; DB 12; Length 47; Pred. No. 3.5; 40; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER EADADELE FORX:
MEDIUX TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ANIXON, HATGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gonsalves, Dennis
Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/039,112
FILING DATE. 31-Dec-2001
CLASSIFICATION: «UKNCWA">
PRIOR APPLICATION OFFER: US 6009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISCRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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                                                           Query Match 8.0%; Score 79; Best Local Similarity 21.0%; Pred. No. Matches 43; Conservative 40; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                             169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                 452 MACAIAIKS-----ANLRRKG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10039112
Publication No. US20030198942A1
GENERAL INFORMATION:
ORGANISM: Grapevine Leafroll Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (716) 263-13(
TELEFAX: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16:
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STATE: New York
COUNTRY: U.S.A.
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                     US-10-138-842A-16
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Gaps

62;

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APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE RPERENDER: 1018-105-999
CURRENT APPLICATION NUMBER: US/16/032,585
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEC ID NO 7808
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                                                      302 EPITEALQIN------ARLRRLVLSKGGSQTPRDMGNMIVAMIQLFVLYSTVKNISVK 353
                                                                                                                         ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                   ------AEDSYLAADFLGTCPKLSELQQSRKM 168
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63
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                                                                                                                                                                                                                                                                                                  US-10-156-761-11789
Sequence 11789, Application US/10156761
Sequence 11789, Application US/10156761
Seblication No. US20030119018A1
SEMERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
SAPLICANT: IKEDA, HAROO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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APPLICANT: GLAG, MAKEL
APPLICANT: GLAG, XUME;
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: TRERAPY OF PROSITIONS, KITS, AND
TITLE OF INVENTION: TRERAPY OF PROSITIE CANCER
TILE OF INVENTION: TRERAPY OF PROSITE CANCER
TILE OF INVENTION: TRERAPY OF PROSITE CANCER
TILE REPERENCE: MRI-044
TILE OF INVENTION: TRERAPY OF PROSITE CANCER
TILE REPERENCE: MRI-044
TILE OF INVENTION UNMER: 6/307,982
PRIOR APPLICATION NUMBER: 6/307,982
PRIOR PELING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
NUMBER: 6/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER: 6/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER: 6/56
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 GAGQFARYEAVLRKVAD-CAPVPLLVPIGERF--DVGALGRVDALLVCGGLTPAYQDALA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 EVEKMINQKGAPNEGIEVVFGILLYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.5%; Score 74.5; DB 15; Best Local Similarity 28.3%; Pred. No. 5.5; Matches 39; Conservative 12; Mismatches 48;
                                                          APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, NASAHIRA
TILLE CINVENTON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILLOCATION NUMBER: US/10/156,761
CURRENT FILLNG DATE: 2002-05-29
FRIOR FILLNG DATE: 2001-08-00
PRIOR FILLNG DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 377, Application US/10205823
Publication No. US20030108963A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces avermitilis
US-10-156-761-10849
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APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Kumei
                                        IKEDA, HARUC
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APPLICANT:
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ORGANISM:
                                  APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21531 VYTVEAKNASGSAKAEIKVKVODIPGKVVGPIRFTNITGEKMTLWWDAPLN---DGCAPI 21587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 LAARTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKL-RTFGRTF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 LAARHGQAWVTTGDPR-LYENGTPEQSVQAIRGQABKLADACAAIGRDVKELDKVLLTGF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LYALAARITS-----PKVQRADSDVI----FSNSFGERNVVVTEGDLKKVLDGCAPL 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09759508B
Publication No. US20020182599A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fishman, Mark C.
TILLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REPERENCE: 00786/381002
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US/09/759,508B
PRIOR FILING DATE: 2001-01-12
NUMBER: OF SEQ ID NCS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 TPDRGRPLESLDAFVDF--AGRH------MELGITCIAIHWPIPDSDFAAD 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
7.7%; Score 76.5; DB 15; Length 3
Best Local Similarity 30.1%; Pred. No. 4.4;
Matches 34; Conservative 12; Mismatches 38; Indels
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Best Local Similarity 22.3%; Pred. No. 3.9e+03;
Matches 39; Conservative 27; Mismatches 67; Indels
                  APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITUE OF INVENTION: NOVEL POLYNCIEDTIDES
FILLS REFERENCE: 249-262
CURRENT FILLION NUMBER: US/10/156,761
CURRENT FILLION NUMBER: JP 2021-204(89)
FRICR FILLION DATE: 2001-65-30
FRICR FILLION DATE: 2001-65-30
FRICR FILLION DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT CARANISM: Streptomyces avermitilis US-10-156-761-11789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1
SEQ ID NO 2
      SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-10849
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APPLICANT:
APPLICANT:
APPLICANT:
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Length 292;

us-09-613-486-15.rapb

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 TEGRIFIEAYVDFCIAYKHKLPQINAAAELGIPAEDSYLAADFIGTCPKLSELQQSRKMF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SNLVITDASSLNGVDKKLLSA-EVEKMIVQKGAPNEGIEVVFGLLLYALAARTISPKVQR
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APPLICANT: Mangold, Beverly L.
APPLICANT: Aldrich, Jennifer L.
APPLICANT: O'Brien, Thomas Specific Antibodies
TITLE OF INVENTION: Anthrax Specific Antibodies
FILE REFERENCE: 38632.0033
CURRENT APPLICATION NUMBER: US/09/844,281
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 6//200,505
PRIOR APPLICATION NUMBER: 6//200,505
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 73.5; DB Best Local Similarity 21.4%; Pred. No. 14; Matches 42; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 -ADSDVIFSNSFGERNVVVTE-------
                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUK:
APPLICANT: SAKAKI, YOSHIYUK:
APPLICANT: SAKAKI, YOSHIYUK:
APPLICANT: BATARYOSHI
APPLICANTON NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-02
NUMBER OF SEO ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptomyces avermitilis
US-10-156-761-12518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09844281; Patent No. US20020082386A1; GENERAL INFORMATION;
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   Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 833
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                          130 DGRLVEYDIDEVVYDEDSPYQNIKILHSKÇFGNIL-----ILSGDVNLAESDLAYTRAI 183
                                                                                                                                                                                                                                                                                                                                                                                                                        80 -----GERNVVVTEGD-----LK-----KVLDGCAPLTRFT--NKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 MGSGKEDYTGKDVLILGGGDGGILCEIVKLKPRANTMVEIDQMVIDGCKKYMRKTCGDVL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 RTFGRIFTEAYVDFCI-----AYKHKLPQLNAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 DNLKGDCYQVLIEDCIPVLKRYAKEGREFDYVINDLTAVPISTSPEBDS--TWEFLRIIL 301
                                                                                                                                                                                                                                                                                                  24 DKKLLSAEVEKMLVÇKGAPNEGIEVV----FGLLLYALAARTTSPKVÇRADSDVIFSNSF 79
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Patent No. US20020552308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
APPLICANT: PA.06
FILE REFERENCE: PA.06
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: 60/24,270
PRIOR APPLICATION NUMBER: 60/24,270
PRIOR APPLICATION UNMER: 20/3
SEQ ID NO 1385
LENGTH: 399
                                                                                                                                                                             Length 368;
                                                                                                                                                                          7.5%; Score 74; DB 15; Length 368
22.5%; Pred. No. 8.9;
tive 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 74; DB 9; Length 399;
22.5%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 DLSMKVLKODGKYF-----TQGNCVNLTEALSLYEEQLGR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 KLS--ELQQSRKMFASMYALKTEGGVVN-TPVSNL--RQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               707
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Best Local Similarity 22.5%
Matches 50; Conservative
                                                                                                                                                                                Query Match
Best Local Similarity 22.58
Matches 50; Conservative
                        ; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-925-301-1385
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US-10-156-761-12518
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SEQ ID NO 377
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Length 451;

Indels

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                                                   43; Gaps
  Length 833;
                                                   Indels
Query Match 7.4%; Score 73.5; DB 9;
Best Local Similarity 24.7%; Pred. No. 34;
Matches 53; Conservative 29; Mismatches 90;
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; Sequence 12518, Application US/10156761

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                                                      TTSPKVQRADSDVIFSNSFGERNVVVTEGD---LKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                        118 AYVD----FCIAYKHKLPQLNAAAELG---IPAEDSYLAADFLGTCPKLSELQQSRKMF- 169
                                                                                                                                                                                              510 QYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTG--NDVGEGTVHFQ 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 KSSTTQQQGGGQGGPGGGTSTGQPQVQGGGASFDV---NSYSVAGVDVTHQDL----- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 APLTRFTNKLRIFGRIFIEAYVDFCIAYKHKLPQENAAAE-------G 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PKVQ--RADSDVIFSNSFGERNVVVTEGDIKKVIDGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 SDSNLSNLVITDASSLNGVDKKLLSAEVEKMJVQK-----GAPNEGIEVVFGLLLYALA
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                                                                                                                                                                                                                                                            170 -----ASMYALKTEGGVVNTP---VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                           568 NGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQ 602
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Publication No. US20330119018A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIEKAWA, JUN
APPLICANT: SHIEKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVA
APPLICANT: SAKAKI, YOSHIVA
APPLICANT: SAKAKI, YOSHIVA
APPLICANT: SAKAKI, YOSHIVA
APPLICANT: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-32
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptomyces avermitilis
US-10-156-761-13439
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Best Local Similarity
Matches 54; Conserva
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US-10-156-761-13439
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US-10-032-585-7518
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                                                                                                                                                                                                                                                                                                                                                                                          21 NGVDKKLLSAEVEKMLVQKGAP-----NEGI-----EVVFGLLLYALAARTTSPKVQRA
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         52;
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7.4%; Score 73; DB 12;
Best Local Similarity 21.4%; Pred. No. 1.4e+02;
Matches 46; Conservative 29; Mismatches 88.
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FILE REFERENCE: 10182-065-999
CURRENT PELLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 75:8
LENGTH: 1987
                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Candida albicans
US-10-032-585-7518
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Job time : 30 secs
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GLRāv-S coat prote Erysipelothrix rhu E rhusiopathiae pr Erysipelothrix rhu Erysipelothrix rhu

AAY97690 AAB14800 ABB07787 ABB08869

AAY95782 ABB54251 ABP29995 ABP25672

Arabidopsis thalia Arabidopsis thalia Putative P. abyssi Phage abortive inf GLRAV-5 coat prote

AAG20733 AAG39165

AAW17788

AAB96072

Lactococcus lactis
Streptococcus poly
Streptococcus poly
Rat hemidesmosome

Lactococcus lactis Candida albicans e Novel human secret

E. rhusiopathiae's Herbicidally activ Grapevine leafroll NADH oxidase. Amp

Grapevine leafroll Drosophila melanog

Propionibacterium Enterococcus faeca

AAW26584 AAU49697 AAU35128 AAW21643

ABB54384 ABP73971 AAU30591 AAW73481 AAR47583

ABB57835

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84.5
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Grapevine leafroll
                                                                                                                     ; Search time 41 Seconds
(without alignments)
765.533 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Side | Animal | Ani
                                                                                                                                                                                                                            1 MELMSDSNLSNLVITDASSL..........GGVVNTPVSNLRQLGRREVX 198
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                                                                                                                                                                                                                                                                                                                                                         1107863
              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAR72682
ABG93273
ABB91963
                                                                                     sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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991
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Match Length
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                                                                                    protein search,
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Perfect score:
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Maximum DB seq
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                                                                                    OM protein
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No.
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Streptococcus DDP Synechococcus CLPB Human titin (conne Human RGS11 protei Beta-TRCP.N/SKP2.C Rat laminin 5 poly Rat laminin 5 poly Herbicidaily activ Human cancer assoc

AAY43219 ABB91943 ABB91943 AAM51651 AAM51651 AAU05396 ABG74786 ABG74786 AAB48461 AAB48460 AAB48460 AAB43940 AAB43940 AAB413940

448 1694 1725 359

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

ALIGNMENTS

AAG10780 AAG10779

399 332 355 367

Grapevine leafroll virus (type 2) proteins and polypeptides - and GRLaV-2; closterovirus; grape; tobacco; transgenic plant; disease resistance; virus resistance; beet yellows virus; tristeza virus; coat protein. Grapevine leafroll virus type 2 coat protein. Ą. ζ. AAW73482 standard; Protein; 198 Grapevine leafroll virus type (CCRR) CORNELL RES FOUND INC 98WO-US10313 97US-0047194 29-MAR-1999 (first entry) Gonsalves D, Ling K, WPI; 1999-045307/04. N-PSDB; AAV08870. WO9853055-A1 20-MAY-1998; 20-MAY-1997; 8661-VON-92

C. albicans BAX-as Herbicidally activ Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Herbicidally activ

AAG39167 AAG20734 AAG39166 ABB91962

AAG20735

0 W 4 W 0 V D 0

Sugar beet yellows

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TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLIRFINKLRIFGRIFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECLAYMHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR 60
                                                                                                   This is the amino acid sequence of a 22 kDa coat protein that is encoded by open reading frame ORF6 (see AAV08B7C) of grapevine leafforl virus type 2 (GLRAV-2) RNA (see AAV08B7C) of grapevine coat proteins 4 (see AAV08B6T-2) for a genome includes 9 open reading frames (see AAV08B6T-2) for a genome includes 9 open reading frames (see AAV08B6T-2) for a polyprotein, an RNA-dependent RNA polymerase, heat shock proteins, coat proteins of unknown function (see AAW13476-84). These can be used proteins of unknown function (see AAW13476-84). These can be used to produce probes and primers for secting molecules can be used to produce probes and primers for secting molecules can be used to produce probes and primers for secting vitis, Agrobacterium tumefaciens, grape, citrus, beet or tobacco citris, Agrobacterium tumefaciens, grape, citrus, beet or tobacco citris, and produce transferm host ceils (claimed). They can be used to impart diama-2 resistance to vitis scion or rootstock cultivars or nicoteance to plants or inspart beet yellows virus resistance to beet cultivars or thisteza vitus resistance to citrus scion cultivars (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
encoding DNA, useful e.g. to impart grapevine leafroll resistance grape and tobacco plants and detect grapevine leafroll virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 198;
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Pred. No. 2.4e-100;
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                                                                   Claim 12; Page 44-45; 151pp; English.
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198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                 67 ORADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bax; Bax_resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death.
                                                                                                                                                                                                                                                                                                                                                                    11 ATFENVSLADOTCLHGEDCDKLRKNFEECLKLKGVPEDNIGIALGLCLYSCATIGTSNKV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid sequence of the novel sugar beet yellows virus (SBYV) capsisd protein. The protein has mol. wt. 22.2 kb. The corresponding gene was obtained from preverse transcribed RNA isolated from purified SBYV. The fragment is useful for the production of virus resistant transperic plants by genetic engineering methods. "Jpdated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                           71 NVQPTSTPIXASPGGGKELYLTHGELNSFLGSQKLLEGKPNKIRCFCRTFQKDYISLRKE
                                                                                                                                                                                                                                                                                                                                         7 SNLSKLVITDASSLNGVDKKLLSAEVERYLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                              ..
                                                                    Sugar beet yellows virus cDNA fragment encoding capsid protein useful for production of virus-resistant transgenic plants
                                                                                                                                                                                                                                                                                    Length 204;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reekmans RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. albicans BAX-associated protein fragment SEQ 1D 504
                                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                 28.9%; Score 286; DB 16; 37.6%; Pred. No. 6.2e-23; iive 29; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eberhardt I, Luyten WHML,
Karasev AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG93273 standard; Protein; 499 AA
                                                                                                           Claim 1; Column 7-10; Spp; Russian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000, 2000EP-0870318.
04-JAN-2001, 2001EP-0870002.
09-JAN-2001, 2001EP-0870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-2001, 2001WO-EP15398
Arganovskii AA, Boiko VP,
                                                                                                                                                                                                                                                                        uery Match
est Local Similarity 3/.u.
-hes 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 VSNIRCLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 VTSIKOLGR 198
                          WPI; 1995-113715/15.
N-PSDB; AAQ87853.
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                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG93273;
                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                              Matches
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preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as concer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMASWKLGPVJATGSTTVLKTAESTPLSALYLSQLLVEAGMPKGVINIVSGFGATAGAAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 FTEAYV------DFCIA-----YKHKLPQLNAAAE---LGIP-AEDSYLAADFL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 IONIIVSIFYNSGEVCCAGSRILIGSGVYDQVVEKFKEAAESVKVGNPFDEDTFYGA--- 343
                                                                                                                                                                                                                                  This invention describes a novel nucleic acid representing a synthetic bax gene. The Bax gene of the invention is useful for identifying Bax resistant yeast or fung; identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually eading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax.induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     vasotropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LMSDSNLSNLVITDASS-LNGVDKKLLSA-EVEKMLVQKGAPNEGIEVVFSLLLYALAAR 60
New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ITSPKVQRADSDVIFSNSFGERNVVV---TEGDLKKV---LDGCAPLIRFINKLRTFGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AKHPKIEK----VAFTGSTATGKIIMKLAAESNLKKVTLELGGKSPNIVFND--ADLDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.0%; Score 89.5; DB 23; Local Similarity 25.1%; Pred. No. 0.82; es 53; Conservative 39; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbicidally active polypeptide SEQ ID NO 1174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- QVSOVQLS-KILKYVESGKSQGATVVT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICPKLSELÇQSRKMFASMYALKTEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                              Claim 36; Figure 2; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB91963 standard; Protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WC-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200210210-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 LEHHNKDSVLYNEKLOKLLPQIEASLPG-SKFLYADVYN--PMMEMIONPSK----YGF 266
                                                                                                                                                                                                                                 The invention relates to identifying target proteins (ABS90797-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 IIDASSLNGV-----DKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFISGYODFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEAYVOFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYAL
                                                                                                                          Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing mucleic acid or amino acid sequency plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 328;
                                                                                                                                                                                                      Claim 5; SEQ ID NO 1174; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 23037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 86.5; DB 25.8%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
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28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.84
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-TEGGVVNT 184
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                                                                                                                                                                                                                                                                                                                                                               useful as herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination sequence
                                                                                            WPI; 2302-269010/31
                                                                                                                                                                                                                                                                                                                                                                                              328 AA;
                               (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
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                                                                                                                        Identifying
                                                              Tietjer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                          organisms
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
AAG20735
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12;

Gaps

43;

3US-3125788	OUS-0126264	JUS-0126785	9US-0128234	9US-0128714	9US-0129845 9US-0130077	9US-0130449	9US-0130510	3US-013U891	9US-0132048	9US-C132407	9US-0132484 9US-6132485	OUS-0132486	9US-0132487	705 - 0132863 205 - 0132863	OUS-0134218	OUS-0134219	9US-0134221	9US-0134268	9US-0134941	9US-0135124	9US-0135353	9US-0135629	905-0136021	9US-0136782	9US-0137222	9US-0137528	908-6137502	9US-0138094	9US-0138540	9US-0138847	9US-0139452 9US-0139452	9US-0139453	9US-0139492	9US-0139454	9US-C139455 9US-C139456	9US-0139457	975-0139458	9US-0139459	9US-0139461	9JS-0139462	9US-0139463	9US-0139763	9US-0139817	9US-0139899 975-0140353	9US-0140354	9US-0140695	9US-C140823	9US-C140991	9US-014128/	9US-0142154	9US-0142055	9US-0142390	9CS-0142803	9US-0142977	9US-0143542	99US-0143624. 99US-0144005.	
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26.5%; Pred. No. 1.2;
tive 23; Mismatches 93; Indels
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99US-0154039.
99US-01554139.
99US-01556139.
99US-0155659.
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99US-0156458.
99US-0156458.
99US-0157117.
99US-01571175.
99US-0158029.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0144335.
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99US-0145085.
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20.-AuG-1999;

21.-AuG-1999;

22.-AuG-1999;

23.-AuG-1999;

25.-AuG-1999;

27.-AuG-1999;

27.-AuG-1999;
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137 SEQPNYFKSYIARLKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRRLEYPFISG 196
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99US-0151930.
99US-0153059.
99US-0153076.
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99US-0161993.
99US-0162142.
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ABB91962 standard; Protein; 360 AA.

ABB91962

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                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying target proteins (ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences to manno acid sequences using suitable search parameters, where plant sequences having an E-value sequences are selected of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                SEQ ID NO 1173.
                                                       Herbicidal; plant; agriculture; herbicide
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                               Herbicidally active polypeptide
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                                                                                                                                                                         28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                              WPI; 2002-269010/31.
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Matches 49; Conserv
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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01-SEP-1999; 99US-0151930.

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905-0140635 905-0140623 905-0140823 905-0141287 905-0141287 905-0142863 905-0142356 905-0142360 905-0142360 905-0143542 905-0143542 905-0143624 905-0143624	905-01443289 905-01443289 905-01443339 905-01443339 905-01443339 905-01443339 905-0144339 905-0144884 905-0145989 905-0145989 905-0145989 905-0145989 905-0145989 905-0145989 905-0145989 905-0145989 905-0145989	9903-6-146389, 9903-6-147038 9903-0147038 9903-01471302, 9903-01471303, 9903-0147416, 9903-0147416, 9903-0147416, 9903-014834, 9903-014834, 9903-014834, 9903-014834, 9903-014836, 9903-014936, 9903-0149426, 9903-0149723, 9903-0149736, 9903-0149736, 9903-0149736, 9903-0149736, 9903-0149736, 9903-015066, 9903-015066, 9903-015066, 9903-0151066,
3. UW. 1999 4. UW. 1999 9. UW. 1999 9. UW. 1999 10. UW. 1999	9-40L-1999 9-40L-1999	02-AuG-1999; 04-AuG-1999; 05-AuG-1999; 05-AuG-1999; 06-AuG-1999; 06-AuG-1999; 06-AuG-1999; 06-AuG-1999; 11-AuG-1999; 12-AuG-1999; 13-AuG-1999; 13-AuG-1999; 13-AuG-1999; 20-AuG-1999; 20-AuG-1999; 21-AuG-1999;
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25-AUG-1999;
26-AUG-1999;
18 - JUN - 1999;
18 - JUN - 1999;
21 - JUN - 1999;
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       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 48419.
                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0121825.
99US-0123180.
99US-0125788.
99US-0125788.
99US-0125788.
99US-0126654.
99US-0126654.
99US-0126623.
99US-0130617.
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99US-01306149.
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99US-0132486.
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99US-01342487.
99US-01342487.
99US-01346602.
99US-0134660.
99US-0134658.
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                          18-OCT-2000 (first entry)
                                                                                                                                                                                                                            Arabidopsis thaliana
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centifizade.

Note: This patent is in the same patent family as WO200065C62, which contains additional sequences as shown in AAB899132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VVTEGDLKKVidGCAPLTRFIN-KLRTFGRTFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide sequences isolated from Pyrococcus abyssi encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86; DB 22; Length 447;
Pred. No. 1.7;
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                                                                                                                                     Hyperthermophilic archaeon, hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                         Forterre P, Thierry JC, Prieur D, Dietrich J, Squerellou J, Weissenbach J, Saurin W, Heilig R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 EAYVDFCIAYKHKLPQLNAAAEL--GIPAEDSYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VHHLLTHSSGIPSLGYAEAFIDGMVGGDNWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Pages 693-694; 1657pp; French.
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                          AAB96072 standard; Protein; 447 AA.
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                                                                                                          Putative P. abyssi beta-lactamase.
                                                                                                                                                                                                                                                                                                                                                                                                                         proteins useful in industry -
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Pest Local Similarity 26.00.
Pest Local Operative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 AA;
                                                                                                                                                                Pyrococcus abyssi
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                                                                               29-CCT-2001
                                                                                                                                                                                                                   27-CCT-2000.
                                                     AAB96072;
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AAW17788
RESULT 12
AAB96072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFCLEHHN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DFCIAYKHKLPQLNAAABIGIPABDSYLAADFLGTCFKLSELQQSRKMFASKYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 KDSVLYNEKLONLLPQIEASLPG-SKFLYADVYN--PMMEMIÇNPSK-----YGFKETKR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2C; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.7%; Score 86; DB 21; Best Local Similarity 26.5%; Pred. No. 1.3; Matches 49; Conservative 23; Mismatches 93
                                                                                                       99US-0153758
99US-0154719
99US-0154739
99US-0154739
99US-0155466
99US-0155659
99US-0155659
99US-0157753
99US-0157753
99US-0158029
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990S-0151930.
990S-0152363.
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99US-0160981.
99US-0160989.
99US-0161404.
99US-0161405.
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990S-C161359.
990S-C161360.
990S-O161362.
990S-O16192C.
990S-O161922.
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                                   30-AUG-1999
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16-SEP-1999
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29-OCT-1999;
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N-PSDB; AAA91259.
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              WO200105957-A2
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                                   25-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 FIDYCVNEEHLGNKGAIKCIFPVI-----TNTLKQKKVDTKXI-DNIFSKRNMVTNFN 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRaV-5; grapevine leafroll virus; GLRaV infection; GLRaV coat protein; GLRaV HSP70 homologue protein; viral gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVERMLVOKGAPNEG-IEVVFGLLLYALAARTTSPKVORADSOVIFSNSFGERNTVVTEG
                                                                                                                                                                                                                                                                                                   Isolated DNA encoding the AbiE protein of Lactococcus - for protecting strains used in production of fermented dairy products
                                                                                                                                                                                                                                                                                                                                                                                                                                               8.6%; Score 85; DB 18; Length 599;
24.3%; Pred. No. 3.3;
Live 26; Mismatches 46; Indels
                      AbiE; abortive phage infection protein; phage resistance; pSRQ800; lactic acid bacterium.
                                                                                                                                                                                    Vandenbergh PA;
                                                      Lactococcus lactis subsp. lactis isolate Wl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 VFEKILDLSLKDSRLTNKFLTFFENINE
Phage abortive infection protein AbiE
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                                                                                                                                          95US-0565907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                               (UNIT ) QUEST INT BV
                                                                                                                                                                                                                    1997-319765/29.
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es 36; Conserv
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                                                                                                                                                                                             Vedamuthu ER;
                                                                                                                     20-NOV-1996;
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                                                                            WO9720917-A2
                                                                                                12-JUN-1997
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This sequence represents a grapevine leafroll virus (GLRaV-5) protein construct of the invention. The DNA sequence can be used in an expression construct. The construct is useful for providing resistance to GLRaV infection in a recombinant plant cell by transforming the plant cell with it, where transcription of the polymucleotide sequence interferes with a normal viral function such as movement, encapsidation or replication of viral RNA. The polymucleotide sequence is expressed as an antisense viral RNA. The polymucleotide sequence is expressed as an antisense cat encodes a GLRaV coat protein, preferably a defective GLRaV coat protein or edication of useful for the synthesis of GLRaV, as diagnostics and probes, for viral seem mapping and for induced plant disease resistance. It is also useful to detect and quantitate expression of GLRaV in plant tissue prior to use in vegetative propagation, by detecting the presence of GLRaV RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protective polypeptide antigen; PPA; Fulisawa strain; swine erysipelas; recombinant production; immunogenic; subunit vaccine; transmucous administration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel grapevine leafroll virus polynucleotide useful as diagnostic and
probe, for viral gene mapping and for induced plant disease resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erysipelothrix rhusiopathiae protective polypeptide antigen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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24.4%; Pred. No. 1.2;
tive 21; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14800 standard; Protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erysipelothrix rhusiopathiae
                                                                                   99US-0144453.
19-JUL-2000; 2000WO-US19708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.4%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-2000 (first entry)
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31-JUL-2000

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This sequence represents a 46.5 kD immunogenic fragment of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix this loperthiae. This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Brysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant protective polypeptide antigen useful as a vaccine for protecting livestock against Erysipelothrix rhusiopathiae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.2%; Score 81.5; DB 21; Length 402;
Best Local Similarity 24.8%; Pred. No. 4.5;
Matches 33; Conservative 21; Xismatches 50; Indels 29
                                                                                                                                            (NORQ ) NORINSUSANSHO KACHIKU ELSEI SHIKENJOCHC.
(HGBT ) HIGETA SHOYU KK.
(FUJI-) FUZITA GAKUEN.
                                                                                                                                                                                                                                                                                                             WPI; 2000-551432/51.
N-PSDB; AAA72313, AAA72317, AAA72318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 14-15; 23pp; Japanese.
99JP-0094004
                                                                      99JP-0094004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  administration.
31-MAR-1999;
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7, 2003, 14:48:31 Search completed: November Job time : 42 secs

60 RITSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFT--- 116 -----EAYVDFCIA----YKHKIPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQS 165

176 AEVNYLPEAHEDFLVSDSSEYNDKLNNINFALGLGVSEFIDY------NRLENMMEX

166 -- RKMFASMYALK 176 ELHPLYLELYANR 239

117

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AF11406 Grapevine
AF11406 Grapevine
AF056575 Beet yellow
AF056575 Beet yellow
X73462 Beet yellow
X73476 Beet yellow
X73476 Beet yellow
X73476 Beet yellow
A41914 Sequence 1
U51931 Beet yellow
A41914 Sequence 1
U51931 Beet yellow
AF0184116 Citrus tr
AF142894 Citrus tr
AF142896 Citrus tr
AF142896 Citrus tr
AF142896 Citrus tr
AF12896 Citrus tr
AF12896 Citrus tr
AF12899 Citrus tr
AF12890 Citrus tr
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AF456773 Citrus t
AF501868 Citrus t
AY190048 Citrus t
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Y14131 Grapevine
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AF339088 Citrus
                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                  Description
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CTR297732
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AR138299
GLAV4131
AF190581
BYU7.295
BYWBPA
CLBYV3PH
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AF342894
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CTU16304
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AF184118
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AF339088
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AF456773
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em_htgo_mus:*
em_htgo_other:*
              htg_hum:*
htg_inv:*
_htg_other:*
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htg pln: *
htg rod: *
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                                                                                                                                                                                                                                                                                                                               9
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-Q=(cgn2_1/USPTO_spool/US09613486/runat_07112003_120411_27395/app_query.fasta_1.391
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-DB=GenEmbl -QFMT=fastap -SUFFIX=+rge -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRMT=pto -NORM==stx + HERASIZE=560 -MINLENS=0 -MAXIX=200000000
-USRE-US09613486 GCGN i 1 3509 @runat -DINLENS=0 -MAXIX 20411_27095 -NCPU=6 -ICPU=3
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-NO_NM=20 -LARGEQÜERY -NEG-SCORES=0 -MAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6
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                                                                                                     20:29:33; Search time 3510 Seconds (without alignments) 2307.723 Million cell updates/sec
                                                                                                                                                                                                 1 MELMSDSNLSNLVITDASSL.......GGVVNTPVSNLRQLGRREVM 198
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                         nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                            2888711 segs, 20454813386 residues
                                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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0.7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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991
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Maximum DB seq
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Perfect score:
                                                                                                                                                                                                                                Scoring table:
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                                                                         OM protein
                                                                                                                                                                                                 Sequence:
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                                                                                                       Run on:
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DEFINITION

AR138306

ACCESSION VERSION KEYWORDS SCURCE

RESULT 2

421 191

481 181

55

121

361 141

101 301

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closterovirus type member
č. Gen. Virol. 79 (Pt 5), 1289-1298 (1998)
98264537
                                                                              Grapevine leafroll-associated virus 2
Grapevine leafroll-associated virus 2
Viruses; ssRNA positive-strand viruses,
Closteroviridae; Closterovirus.
1 (bases 1 to 15000)
Zhu,H.Y., Ling,K.S., Goszczynski,D.B., M.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                           GI:3123909
                                                                                                                                                                                                                                                                                                                                                                     .15000
                                                           AF039204.1
                                                                                     SCURCE
ORGANISM
                                                                                                                                                                                                                                                                                                         TITLE
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MEDLINE
PUBMED
                                          ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                           TITLE
   16-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluArgAsnValValValTnrGluGlyAspLeulysLysValleuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuThrargPheThrasnLysLeuargThrPheGlyargThrPheThrGlualaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsoPheCyslleAlaTyrLysHisLysLeuProGlnLeuAsrAlaAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLeuGlnGlnSerArgiysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlyValAsplysLeuLeuSerAlaGluValGluLysMetLeuValGluLysGly 40
                                                                                                                                                                                                                                                                                                                                                                                                          MetGlubeuMetSerAspSerAspbeuSerAspLeuVallleThrAspAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGCTCTAAAAACTGAAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValWet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.

1 (bases 1 to 597)

1 (bases 1 to 100 kg.)

Buth.H.-Y., Ling,K., and Gonsalves,D.

Grapevine leafroll virus (type 2) proteins and their uses

Patent: US 6197948-A 14 36-WAR-2001,
                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
AR138306 597 bp
Seguence 14 from patent US 6197948.
                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                (1-597)
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                  /organism="unknown"
121 c 157 g
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                                         GI:14479815
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100.00%
100.00%
                                         AR138306.1
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Best Local Similarity:
Query Match:
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                             AR138306
                                                                     Unknown
                                                                                       Unknown.
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Pred. No.:
Score:
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DB:

source BASE CCUNT ORIGIN

AUTHORS TITLE JOURNAL FEATURES

ORGANISM

REFERENCE

21

61 41 121 181

8 241

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VETERADARA VEREARAGGS VETERADARA VETERAGENER VETERADARA VETERA VETE /1. 7423
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/note="larger than 277 kDa; ORFla; contains domains for
/note="larger than 277 kDa; ORFla; contains domains for
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a helicase; lant="dentified by sequence comparison"
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CDS

m

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13084 ATGGAGTTGATGTCCGACAGCAACCTTAGCAACCTGGTGATAACCGACGCCTCTAGTCTA 13143
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GIEVVPGLLJYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLT
ELQGSRRWFASNYALKTEGGVNNTPVSNLRQLGRREVM"
13680. 14165
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FWFPLRSETKGRAVRH:LRTFFEANNFFFGSHCGTMEYCLKQVLTETESIIDSFCEERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MRVIVSPYEAEDILKRSTDMLRNIDSGVLSTKECIKAFSTITRD
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PVKIFRDLLLDVETLNELCAEDDVHVDKVNEMGDENHILELQDEC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14785. .15000
/note="similar to 3'UTRs of other monopartite
                                        ccat protein"
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Matches:
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                                           diverged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/db_xref="GI:3123915"
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                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/product="RNA-dependent RNA polymerase"
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DEELLAIWMCGERLSIANTLDGGLSFTIENQRKSGASNTWIGNSLYTLGILSLYYDVR
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YLGSTDLFFTAPDFILDLATGILYDECKEYNVFYSSYKRNVDNSFELANYMPJ.SOYRT
YLGSTDLFFTAPDFILDLATGILYDECKEYNVFYSSYKRNVDNSFELANYMPJ.SOYRT
YPOWYKPAPDVRLLFEUSAAELTLEVPTLSLIDSQVVVGHILRTYVESYTSDFILDALE
                                                                                      KEVSNIECQKRKDKRSPKKSIYTIDAVLMHRGCDADVLFIDECFWHAĞSVLACIEF
TRCHKVMIFGDSRQIHYIERNELDXCLYGDLDRFVDLQCRVYGNISYRCPWDVCAMLS
TVYGNIATHYGESEGKSSMRINBINSVDDLYPBDVGSFFLCAGSEKLBISKHFIRKG
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RGDATODAIQKAABLYNKFRVFPTSFGGSVIKLNVKKDV9BNSRCKASSAPLGVINDF
LNEVNPGTAVIDFGDLSADFSTGPFECGASGIVVRDNISSSNITDHDKQRV
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FVPDPYKLFVKLGAVKEDVSMDFLFETFTSFKDLTSDFNDBRLIQKLAELVXEVQ
TGNTTLALSVIHCLRSNFLSFSKLYPRVKGWQVFYTSVKKALLKSGCSLFDSFYTPFG
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NYTYVRASGGDLNLGGRDVDRAFLTHLFSLTSLEPBLTLDISNLKESLSKTDAEIVY
TLRGVJQRKRDVRVNKNILTSYMLPVNRTLKILESTLKSYASMNESARVKCDLVLI
GGSSYLPGLABUTTGGSVDRILRNSDPRAAVAVGCALYSSCLSGSGGBLLIDCAAFT
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GANIRFFDIGVTGDSYAPVTFYMDFSISSVGAVSFVVRGPEGKQVSLTGTPAYNFSSV
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DVEKFFDKLQRELPNVSLRRQFNGARAHEAFKI PKNGNI SFRPTSRLNVPREFNYLNT
DYFRHANRSGLTEEEILILNNI SVDVRKLCAERACNTLPSAKRFSKNHKSNI QSSRQE
GLINAVREFYYMGEJALFEIHSKLCTYYDQLRIVNFDRSVAPCSEDACLYVRKNGSTI
VQGKEVRLHIKDFRIPDELFDCKISINKRRRGGNVLYHDNLAFLASNLFLAGYPFSRS
FVFTNSSVDILLYEAPPGGGKTTTLIDSFLKVFKKGEVSTMILTANKSSQVEILKKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="MNQVLQFECLFLLNLAVFAVTF1F1LLVFRV1KSFRQKGHEAPV
PVVRGGGFSTVV"
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                                                                                                                                                                                                                                                                                                                                    cther
                                                                                                                                                                                                                                                                                         /function="replication"
/note="RARp; 52 kDa; similar to RNA polymerases of otheriosteroviruses; presumably expressed via +1 ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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/note="p65; HSP70; similar to heat shock 70 proteins;
identified by sequence comparison"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8865. 9035
/note="6 kDa; probably membrane-associated; similar t
small hydrophobic proteins of other closteroviruses"
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codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AASALPPJEDVELLIGKSVQKVLRGSRLEEIPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC40857.1"
/db_xref="GI:3123912"
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101 LeuThrargpheThrasnLysLeuargThrPheGlyArgThrPheThrGlualaTyrVa; 120 13884 CTCACTAGGTTCACTAATAAACTTAGAACGTCGGTCGTACTTTCACTGAGGCTTACGTT 13943 121 AspPheCysllealaTyrLysHisJysLeubroGlnLeuasnAlaAlaAlaGluLeuGly 140 13944 GACTTTGTATCGCGTATAAGCACAAATTACCCCAACTCAACGCGGGGCGAATTGGGG 14003 141 IleProAlaGluAspSerTyrLeualaAlaAspPheLeuGlyThrCysProLysLeuser 160 14004 ATTCCAGCTACTTAGCTGCAGTTTTTTTGGGTACTTGCCGGAGGTCTCT 14061 14004 ATTCCAGCAAATTAGCTGCAGTTTTTTTTTGGTACTTGCCGGAGGTCTCT 14061 161 GluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180 14104 GAATTACAGCAAAGTAGGAAGTTGCGGGGATACTTACGGAAATTAGGTGGA 14123 1810 ValvalaAsnThrProValsErAsnLeuargGlnLeuGlyArgArgGluValMet 198 1811 ValvalaAsnThrProValsAsAATAGCAGCTAGCTAGGTAGAAGGGAAGTTATG 14177 24124 GTGGTAAATACACCAGTGAGCTAGGTAGGTAGAAGGGAAGTTATG 14177	GLAV4131 Grapevine leafroll-associated virus 2 genes and coat protein, hsp70, hsp90 gene and ORP 144131. Y44131. Grapevine leafroll seasociated virus 2 Grapevine leafroll associated virus 2 Grapevine leafroll associated virus 2 Viruses; ssRNA positive-strand viruses, no closteroviridae; Closterovirus. Abou-Ghanem, N. The nucleotide sequence of the 3 terminal 1 clafroll associated virus 2 closterovirus. Abou-Ghanem, N. The nucleotide sequence of the 3 terminal 1 clafroll associated closterovirus 2 closubulished Babou-Ghanem, N. Shout-Ghanem, N. Birect Submission Submitted (31-701-1997) N. Abou-Ghanem, Jning 1 pign 1 markinem no die pign 1 markinem	Tr Ce	WĪGNSLVTLGILSLYYDVRNFEALYISGDDSLIFSRSEISNYADDICTDMGFETKFMS PSVPYFCSKFVVMCGHKTFFVLDPYXLFVKLGAVKEDVSMDSLFETFTSFKDLTSDFN
8686868686	AESULT 4 GLAV4131 LOCUS DEFINITIC ACCESSION VERSION KEYWCRDS SOURCE SOURCE SOURCE AUTHOR TITLE JOURNAL REBERBING AUTHOR TITLE TITLE TITLE TITLE	REMARK RETEXENCY AUTHOR COMMENT FEATURES SO COM	
	Qy 181 ValValhsnTh-ProValSerAsnieuArgGlnleuGlyArgArgGluVolMet 198 Db 13624 GTGGTAAATACACCAGTGACCAATCTGCGTCAGCTAGAAGGAAAGTTATG 13677 RESULT 3 AR13829 15500 bp DNA linear PAT 16-JUN-2001 LOCUS AR13829 15500 bp DNA linear PAT 16-JUN-2001 DEFINITION AR13829 GI:14479808 AR13829 Uncount Uncount VERSTON AR13829 GI:14479808 AR13829 Uncount ORGANISM Uncount Uncount Uncount Uncount ORGANISM Uncount Uncount Uncount AUTHORS Zhu,HY., Ling,KS. and Gonsalves,D. Location/Qualifiers AUTHORS Location/Qualifiers Location/Qualifiers FEATURES 1.3594.a 1378.c BASE COUNT 1984.a 3178.c ORIGIN 1984.a 3178.c	1.44e-95 Length: 15500	13824 GAGAGGAATGTGGTAGTAACAGAGGTGACCTTAAGAAGGTACTCGACGGGTGTGCGCCT 13883

CDS

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**Cof c 2135 g 2425 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGGTGTCGACAAGAAGCTTTTATCTGCTGAAGTTGTAAAAATGTTGGTGGTGCAGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AlabroAsnGluGlylleGluValValValPheGlyLeuLeuTyrAlaLeuAlaAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCCTAACGAGGGTATAGAAGTGGTGTTCGGTCTACTCCTTTACGCACTCGGGGAAGA
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        ELQQSRKYFASYYALKTEGGVVNTPVSNLRQLGRREVM"
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                             7306. .7791
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VERSION KEYWORDS

RESULT 5 AF314061 LOCUS

22.

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

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CDS
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KLLSARRRKLQQQNFNSRVAKKARDVTASRVDYABGEVTPPRHIFFGSFSEFPIPS
SGMARSVLREBPAITTCGASAPAIKETPRVSVKKADESPAAPVREALITPRVAKRGEA
IVSGVVHEVLNKIREBPAITTCGASPAPIKETPRSTHGCKIVAVYTTNTSVHLNCTVR
NGEKTEVATPIPCSVDYVAMLRYVSGGKFPLVLNSRECYPDGLCYMAHRYLLGAFCCPF
RESDYPLGSWPSVARLKALVLKRFGDEALNIGVRGYYVSRRAFHCDYDSKYARSLINEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGRPPLVLMTRÖKYRNGYCYLAHCRYASAFLLKGFHPAVFLIGANPTAAKLISRRWV
SVLGDRSLEANLYGSFTSGFTHCVPAYVEXLERSBAYASPTTPA
KVGTREAVYDR.YGSFTSGFTHCVPAYVEXLERSBAYASPTTPA
KKYTTEAVYDR.YGSRDSLLK.SIENDLIDFRADVGSELKRRPVIRVPFWSSYTON
SLTRFYPGFELKFSHSTHSDHPAAAASRLLENBTLVRLCGHSVSDIGGCFLFHLNSKT
SKRYHVCRPYDLGKAARRYKRELQYSSWRSODDEKILGGPSNVDVGTFPLGYGCFTSGSTSTHOWVOVYDAS.YSTCSAMIKKARRITYTTMYTDGFFLDGRSCVMSSLDCDJEVDN
HAJVVMYKFGSSCYSHKLSIIKDIMTTPYLVLGGSFLFSVEXYSIRMGVNYFKIIKGSV
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FSSLPITGASFQKIKFTSFSSYSKELALFSSTSLTGFGCFFFRQFPUSP
OCGPLSVCLGCWNG: FAVLL: SFPFLDVASLLADVGDVYTPTKVRISKRAKKLKRAF
SIARAAARIRRSKVGNKEVRISHVQPLPAGGLRFSQNKNGTELLIIGRDVGVVARVKT
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KVLRKVEPRNGVRTESADVGSNVTRKRDARIDRKFSHLLAGSVNKVKKRIAAGVLRYR
VGGDMDFHNSFLTQAGYHLLVRRKTSSSVCVELSTPDGRLLRRDVIPCSRDYAAMLSF
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CSAVNSKTFBWVWSFIKSSKSRVIISGKIIHKDVNLDLKYVESFAAVMLASGVRSRLA
SEYLAKVLSHFSGDCSFIEATSFVLREEIRNMTLNFNECLLGLVKRVAFATLDVSFLD
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VYAKTAENEKSEVSEKKEHKOELGGGSKAGVLKEFLDPVLSSARLEFSCVADQQRIK
SYMYLDTAVSFLDONYENLSFIRMUSKGCOSKAGVLKATUNGSLANRVASAVOIVREI
AVLCANVSVSKAKVVYTFSAAVCAMMYNSCGFSGDGREYKSYMIRYTQVLFDTIFFED
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SEDVADALSSIEECDEIENLIGDGFRDMADDSLTDYNYFDFSDFLASVNGLFCAGLR
GGGRRVGMLAILNYVYNSLSIMARAASKNSTFTSJIIFSRGLVDRIRNIFSNKESVVE
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TATDGVMRSVFSQIISHLVGNTGNLAXQIAFLTGVVPLLVKKCVGLIFSMSEDTYSG
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                                                                                                                                                                                                       VRL 06-NOV-2002
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Grapevine rootstock stem lesion associated virus

metryltransferase/helicase polyprotein, RNA-dependent RNA
polymerase, p6, HSP70-like protein, HSP90-like protein, coat
protein duplicate, coat protein, p19, and p24 genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-CCT-2000) Plant Pathology, University of California, One Shields Ave., Davis, CA 95616, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             grapevine rootstock stem lesion associated
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product="methyltransferase/helicase polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grapevine rootstock stem lesion associated virus Grapevine rootstock stem lesion associated virus Viruses; sgRNA positive-strand viruses, no DNA stage; closterovirided; Closterovirus.

1 (bases 1 to 1652)
Lhang,Y. and Rowhani,A.
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db_xref="GI:24636915"
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'db_xref="taxon:167634"
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note="327 kDa"
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Zhang,Y. and Rowhani,A.
Direct Submission
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Unpublished
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source

FEATURES

CDS

REFERENCE AUTHORS TITLE

JOURNAL

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ENTITIONS OF THE STATE OF THE S CLSAERREKFALVCLVTLGFPYFARFLGGVVCDKLLSSLRRAYDRVIVFLKERCDAA MNGLRCLFHFDGNGDSTSAGLKGGGSQTFLWGLLLRIVRFALSLGYAGCKCVFSHHDL FFLCVSLVBEVNMIAKTLGCLSFFSRRISSALAFALLQPERFVEYSGKLSTTFLFPLK ISPVPLKIKGFFFWVAGSPLLRGVFFLALIAVKLNLERKRGLRTANGGYFSGFAVP VIPSNRVTNGGCERJSEKMGSVFALRSELALLDAAVVSKLNKRRREADTSSFFSP PMHESTHDVTSFCSKANSVGTALBRAVLVSDAVKSEKISRKAKDLVRKGTVSDEITN TLSDDEA! EEVPVSEERDDSPKTVRVSEYLNRLNSSPEFPKPI VVJDNKETGGLTNAV REFYYMQELALFEI HSKLCAYYDQLR I VNFERSMAPCNEDAQL YVRKNGST I VQCKDV RSN I KDFHDHDFLFDGKI SVNRRRRSGNVL YHDNLSFLASNLFLAGYPFSRSFVFTNS SVDILLYEAPPGGGKTTTLIDSFLKVFKKGEVSTMILTAKKSSQVEILKKVEKDISNI ECQKRKDKRTPKKSIYTIDAYLMHHRGCDADILFIDECFMVHAGSVLACIEFTRCHKV MIFGDSRQIHYIERNELDKCLYGDLDRFVDLQCRVYGNVSYRCPMDVCAMLSVVYDNM IATVKGEŠECKSSKRINEINSVODEJVEDMGSŤYLCMLOSEKLEISKHFIRKGLSKLNV LTVHEAQGETYARVNLVRLKFQEDEPFKSIRH:TVALSRHTDSLTYNVLAARRCDATC DAIQKANELVNKFRVFPTSFGGSVINLDVKKDVEDNSRCKASSAPLSV:NDFLSDVNP /protein_id="AaN63467.1"
/db_xref="G1:24636916"
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// Infore=153 Kba; translated via ribosomal frameshift"
// codon start=1
// product="RNA-dependent_RNA polymerase"</pre> GTTVIDFGDLSADFSTGPFECGASGIVVRDNISSSNITDHDKQRV" /product="HSP90-like protein" /protein_id="AAN63470.1" /db_xref="GI:24636919" product="HSP7C-like protein"
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15143
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/note="The polyprotein encompasses domains for papain-like leader proteinase, putative methyltrensferse, RNA helicase and RNA-dependent RNA polymerase (RARp); ORFIa/b; papain-like leader Broteinase is capable of autoproteolytic release from the rest of the polyprotein, and is a replicational enhancer. RARp is presumably expressed via a +1 ribosomal frameshift"
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RHIDFVVNRPFSVFPTEVLSVSSERTPSRLFALLCDFFLYCSKPGPCVEIASFSTPPP
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ALGYTSKRPRSRIQOPPRVRSHKRKINKAVE
PFFFPESPKKDKRKKASLPYTKDEGFIPTFGTLRFPLESTPKEPBRLPKFREVEIPVVKK
HAVPAVVSKPVRTFRPVATTGAEYVMARTQCSRFPRNHILLRSASYTFGFKKMDLOKF
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                                                                                                                                                                                                                                                                                                     161 GlubeuGlnGlnSerArgbysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
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/db_xref="taxon:12161"
/note="Californian strain, RNA transcript derived from this cDNA clone causes formation of red necrotic lesions in Claytonia perfoliate and systemic infection in Nicotiana benthamiana.
//ore.108, 7997,7999, 9381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beet yellows virus
beet yellows virus
beet yellows virus
Viruses; seRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.

1. (bases 1 to 15468)
1. (hases 1 to 15468)
1. (hases 1 to 15468)
1. (haseloviv.v., Hagiwara,Y. and Doija,V.V.
HSP70 homolog functions in cell-to-cell movement of a plant virus
proc. Natl. Acad. Sci. U.S.A. 96 (26), 14771-14776 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 15468)
Peremyslov, V.V., Hagiwara, Y., Alzhanova, D. and Dolja, V.V.
Direct Submission
Submitted (27-250-1999) Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA
Location/Qualifiers
                                                       14984 CTTAATAGATTCACTAACAAGCTGCGAACTTTCGGCCGCACGTTTACGGAGGCGTATGTT
                                                                                                                                                                                                              141 :lePrcAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                                                                                                                                                                                                                                                       15084 GAATTACAACAAAAGTAGAAAAAGTTTGCAAGTATGTACGCTTTGAAGACTGAGGGGGA
                                                                                                                         AspPheCyslieAlaTyrLysHisLysLeuProGinLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                                            15024 ATACCAGCAGAAGATTCGTACCTAGCTGCGAACTTTTTAGGTGCTTGCCCGAAACTCTT
                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Beet yellows virus strain BYV-4, complete genome.
AF190581
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AUTHORS
TITLE
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AUTHORS
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AF190581
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/db_xxef="G1:24634691"
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BLQQSRXMFAGNYTAANTEGGVVNTPVSNLRQLGRREVX"
15200. .15685
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procein_id="AaN63474.1"

/db_xref="GI:24636923"

/translation="MRVIPSYFEAEDILTRSTEMLRNIDSGALDTRECIKAFSTLTRD
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AFITRKYVKLTGVAAREAVKIEMRTLSKTVLNKLSLEMAFYMSPRAMKNAEMLDLRYI
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SHRGDVTGCNREDVIKDFEGAHHTVIRSRTVRYDYESAVKEYNNADCVVKFFLETGDV
FWFFLQSDIKGRAARHLRTFFEBANNFFFGSHCGTMEYCLKQVLIETESVIESFCEERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetGluLeuMetSerAspSerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaProAsnGluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14604 ATGGAGTTGATGTCCGATGATAACTTGAGCGGTCTCGTCATAACGGACGCTTCTAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14664 AATGGTGTCGATAAGAAACTGCTGTCTGCGGAGGTCATAAAAA;GCTTGTGCAGAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLKIYRDLLLDVDTLNALCEEDEIHVVVTNKDEDENHDLELQEDC
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                                                                        protein duplicate'
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAN63473.1"
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                                                                           product="coat
                                                                                                                                                                                                                                                                                                        codon_start=1
product="coat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=:
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                          'note="25 kDa"
                                                  ccdon start=1
                                                                                                                                                                                                                                                                                  "note="22 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="19 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="24 kDa'
                                                                                                                                                                                                                                                            14604. .15200
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921.00
95.96%
90.91%
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Best Local Similarity:
Query Match:
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ORIGIN
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CDS
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LDGLSDGLTHMOVSVPRRLFVALRRALSAYSNBALRRKI FEFF FGNITHPPEVVAVIET
NEVABRPLSPEVDI DVDCDFGSDSESVSSDEVASI PRPGLHGGSRRSSNFLTSLVKVV
KAGARI PRLLFRLBRNFYPRRALSAKRÄKTF FGLARLENDRSLTSVVYLLOEDES
VLINAT I DVELVLLGASSVAVLELVSWYRGS LTKLAEVLVGSGFAS FLGRMCCAVSDM
SSSNAGCNFWSPVRTKGKPVPPSSSGSTASMYERLEAESDIREHVLSTCRVGSDE
ERPREVTEPEDI EHTSEDVVPIRSHOOPLSGECSVSEDRAENBANLI PHYSKI VSE
RRGLSTARRNKTLRGVSSTANATNSNBOPRP I TVDHS PSSRALTNSVRSFYLOEL
ALFELSCKLRRYYGDLKVANFNRQSCLCDKDSDMFVLRAGGSVVSGNNSRLDHVHFKE
HEGERSGGLVPVDGTSRVDTI FHTQTNFVSANALLSGYLS YRTFTFTNLSANYLYE
                                                                                                                                                                                                                                                                          PREDKTIKKT FLISGYDY LYLDAKFVSR VFDY VVSNCS VVNSKTFEWWSY IKSSKSR VV
FREWSRRAY DET INGENERALE WAS VOURSKTTEF MALLINKYTGORSCFETTRFL
FREWSRRAY DET INGENER KLAKES ILSAGLDY BELDLINSL CHILLEY SEVERYSTAGLA
EVOCH BENNY VLTE: I ABBADRK SI AQGLISGALSS VPTOPRGGLEGSRRSGYSFLYNL
BEGYBL FESYGDAWR FLYKPRTFESDES PIR VVRMFLDLEBAASPFSUSVLYGAWLR
EAVGAPSSWYADRT VSEX VKFFVNRTVKR FLAPMSAKTLTKKFFRF.SASALAKTVV
RKAKYI LEAYWEVWFESILSDSGESSS VANTORT KREFRF.SASALAKTVV
RKAKYI LEAYWEVWFESILSDSGESSS VANTORT KREFRF.SASALAKTVV
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SLPVFRKKVALCVPGDMATTARELEGGSVNSTASSALDGS
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SLVALSGVAKERVLDSFKXIIKPLNVFRVNTRTSSSTDLSSDEYBCLDESKPG
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RTIRCAGGFTYLDSBAYDEBMLRQFREQYYSSDESVTYGRFRVLMSRYLNVSRRFL
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ITACECVSQICCLRLIRLGWGTPACGLVRLFYITYSGTRVLSRVVAVANVCPLLVRNB
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ILIIDSYLMANRGJTCKVLYLDECRWHAGAAVACIEFTKOSAILEGDSRQIFFIDR
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QVREIESVDDVEYSSEFVYLTMLQSEKKDLIKSFGKRSSVEKFTVLTVHEAGGET
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RNYNFTVCERFSGPQEFGQAMAMVMLERSFDLEKVAKVRSDVIAITEKGVRTYMSKRE
PSQLRALSSDLQKPLNLEEEITTFKLMVKRDAKVKLDSSCLVKHPPAQVIMFHRKAVN
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GRSYLPGELLSRLSSVPFVYECLULPDRRAAVRAGGALYSGCRDISPRLLVOCAHN
LSISSKYCESIVCVPRGSPIPPTGWRYWAGSNASAVYSAALFEGDFVKCRLIKRIF
SGDVALGDVGVFGSNTRIVPLILEINVSSVGTIIFSLVGPTGVKKLVGGONAAYDFSSY
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SYDDAVLNSSELLLGRVIPKILRGSRVEKLDV"
11311. .12972
LFHCDVASAPSSPFYSLPRFIGGVEEEAPEITSSLKHKAIESVYERVSLHKDNLLARS
VEKOLIDFKOEIKSLSKEKRSVTVPFYMGEAVQSGLTRAYPQFNLSFTHSVYSDHPAA
AGSRLLENETLASYAKSSFSDIGGCPLPHIKAGSTDYHVCRPIYDMKDAQRRYSRELQ
                                                                                                                                  ARGLVENLSREQLVEAQARVSVCPHTLGNCNVKEDVLIYVQVYDASLNETASAAVLKE
SKVAYLTMYT PGELLDEREAFAIDALGCDVVVDTRRDMVQYKFGSSCYCHKLSNI KNI
MLTPAFTFSGNLFSVEMYENRMGVNYYKITRSAYSPEIRGVKTLRYRRACTEVVÇVKL
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AYRVYPTSFGGSTLDISVNPSTSDRSKCKASSAPYEVINSFLESVVPGTTSVDFGDVS
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KSQDAFIKSFERTLYSAFGFDEDLLDVRMQGEYTSNATTLDGGLSFSVDNQRKSGASN
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VDERVIELLTHLVHSKYGYESGDTYAALCAIHCIRSNFSSFKKLYPKVKGWVVFYGKL
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SKSTVRLDCYSGTVPQNATLPGLIATFVKALISTASEAFKCQCTGVICSVPANYNCLQ
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NNTFVVRASGGDMNLGGRDIDKAFVEHLYKKAQLPVNYKIDISFLKESLSKKVSFLNF
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/note="small hydrophobic protein, ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFVLRKFANCFREKFDJAFGEAYFLTYDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF14301.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
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cell-to-cell
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TKRFVSLIFKGKDVVBSTDBAVVSSSYLDYLSHCLNYBTCKNLSSNSGKKALTNPFC
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SELIEMWWEOPAPDVRLLFELDTTELLLKI PTINTHDSTFLYKNKLRYLESYFEDDSN
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13641. .14255
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STELTDLQGGRLLLARENATHTEFSSESPVTSLKQLGRGLATGK"
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KILNRKVTFTFESGI QLVFGMYGRDQRCVSSEYLMFENVFVGAHCGTLPYCLNCELDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAP14307.1"
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SETLNAFLEBYCRITGLIREDALRSHORRVRSTVLFHHSELLKFEVTENMFSFTELLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTSSVELAQTKPLFRVLLLKGFVFYIVAIETEEESPEVELPLVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="enhancer of RNA accumulation"
/note="21 kDa protein; ORF8"
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71
32
84
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/note="ORF5; CPm"

/codon start=1

/product=minor capsid protein"

protein id="NAF14304.1"

/db_xref="GI:6492372"
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Mismatches:
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/db_xref="G1:6492374"
/protein_id="AAF14303.1"
/db_xref="GI:6492371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-613-486-15 (1-198) x AF190581 (1-15468)
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Genes required for replication of the 15.5-kilobase RNA genome
                                                                                                                                                                                                                               GCSACTTTTGAAAACGTGAGTCTCGTAGACCAAACGTGTTTTGCACGGTGAAGACTGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsniysleuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCyslleAla
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                                                                                                                                                                                                                                                                              27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                    GlnArgAlaAspSerAspVaillePheSerAsnSerPheGlyGlu---ArgAsnValVai
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                                                                                                                                                                                                                                                                                                           31 AAACTACGGAGGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGATAAACTC
                                                                                                                                                                                                                                                                                                                                               47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
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1 (bases 1 to 15468)
                                                  Length:
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Conservative:
Mismatches:
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Dolja,V., Peremyslov,V. and

Direct Submission
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Beet yellows virus
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                                                                                                      Similarity:
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Codon_start=1

/product="cost protein"

/protein_id="aAB17001.1"

/protein_id="G1.1619940"

/translation="MGSAEPISAIATENVS;VDQTCLHGBDCDKLRRNFEECLKLKG

/translation="MGSAEPISAIATENVS;VDQTCLHGBDCDKLRRNFEECLKLKG

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OKLLEGKPNKLRCFCRTFQKDVISFAKEYRGRLPPTARANHGLPABDHYLAADFIST

STELTDLQQGRLLLARENATHTEFSSDSPVTSLKQLGRGLATGD"
                         13731 AAACTACGGAGGATTTCGAAGGGTTTGAAAITGAAAITGAAAGGGGTTCCGGAAGATAAAACTC 13790
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Creamer.R., He.X.H., Yang,C.H. and Grantham,G.
Direct Submission
Submitted (19-SEP-1996) Plant Pathology, University of California,
Riverside, CA 92521, USA
Location/Qualifiers
                                                                                                                                     GlnArgAlaAspSerAspValllePheSerAsnSerPheGlyGlu---ArgAsnValVal 85
LeuLeuSerAlaGluValGluLySMetLeuValGlnLySGlyAlaProAsnGluGlyIle 46
                                                                                                                                                                                                                              13791 Gercresegraadaktristristrateresegadaktristrataakir
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                                                                    GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
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1 (bases I to 612)

1 (bases I to 612)

Creamer, R., He, X. H., Yang, C. H. and Grantham, G. Characterization of the 3'-proximal encoded proteins
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/mol_type="genomic RNA"
/isoTate="California BYV-CA"
/db_xref="taxon:12161"
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protein_id="AAC25116.1"
db_xref="GI:3283078"
'translation="MDCVLRSYLLLAFGFWICLFLFCLVVFIWFVYKQILFRNTPPSN
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RSFTESCVNLSGYPCVYMVVEPSAAALSACSRIKGATSPVLVYDFGGGTFDVSVISAL
NNTFVVRASGGDMNLGGRDIDKAFVEHLYKKAQLPVNYKIDISFLKESLSKKVSFLNF
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LSISSKYCESLVCVPAGTPTPTGYRTVNMTGSNASNYYSAALFBGDSVKCRLNKRIF
SGDVALGNVGVSGSNTTRVPTLLEINVSSVGTITFSLVQPTGVKKLVSGNAAYDFSSY
QLGRRVVADLHKHNSDVKL.HALTYKPFQSKKLTEGDXALFKRLSADYRREAGKFS
SYDDAVLNSSELLLGRVIPKILRGSRVEKLDV"
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FRFSNGEVLSRKNFSDSTGESFVREFSLLLTFPKTYEVCKLCGVAMEQALSGKNRLSD
YNVSELNVVDVKTVGCKFNIQTVTEFVRKLNGNLAEPSLVEHCWSLSNSCGELINPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELIKUKUSELLTRDN PELKLAQRWUGFHCYYGVFRTAQTRKUKRDAEYKLPPALGEFT
INMGSVEBEPEDBLQKKAPSVSTRRFCGSLSHEFS I FKRGVGFPPTTRLNUPYKYS
YLNUDYBHVKRAGLTQDE-TILSN: EFDVABMCCRF3VALQARAQRGEKPPGAWG
VKNEVSPHARSIRVKGNNESLLNULMKDVGARRQGRLNPLHRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETDELLGVIRERFKSELVITDEDFVKHLAFALIRAANITTSTKVNYVGAYEYTIGGKK
FLVKJAMVFPLIKECMKKFNKPNPVRTFCATFEDAYIVIARSLPKLFLNRTIGKRGIP
SGYEFLGADFLTATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MGSAEFISAIATFENVSLVDQTCLHGEDCDKLRRNFEECLKLKG
VPEDKLGLALGLCLYSCATIGTSNKVSVQPTSTFIKASFGSGKELFLTHGELRSFLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKRFVSLIFKGKDVVESTDEAVVSSSYLDYLSHCLNLYETCNLSSNSGKKALYDEFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVIVYLETSDLEYRSLSDNPLVAGVLYDMCFZYNTLKSTYLKNIESFDCFLSLYLPLL
SZIFSMNWEQPADDVRLLFELDTTZLLKIPTINTHDSTFLYKNKLRYLESYFEDDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVAFGYDAEVLSNDPSVRGGFYRDLKRWIGCDEENYGDYLEKLKPHYKTELLKVAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVSEQNVKVDVLVNVSBLAEVAAPFVERTIKIVKEVYEKYRGSMRLEPSVKAKLJMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'translation="MLAPEGRGDLIHFTENTRDAMETFFNSYDLAEYSEVNFNKLNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MVVFGLDFGTTFSSVCAYVGEELYLFKQRJSAYIPTFVFLHSD1"
                                                                                                                                                                                                                                                                                                                 product="RNA-dependent RNA polymerase"
note="ORF 1b; presumably expressed via a +1 ribosomal
                                                                                                                                                          product="putative methyltransferase and RNA helicase"
note="ORF la"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ORF 2; p6; small hydrophobic protein"
codon start=1
product="6.4 kDa protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="homolog of HSP70 proteins; ORF 3"
                                                   function="replication enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="minor coat protein"
protein id="AAAC25119.1"
/db_xref="G1:3283081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13641. .14255
/note="22 kDa protein; ORF 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="major coat protein"
protein_id="AAC25120.1"
db_xref="G1:3283082"
                   function="autoproteolysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12920. .13570
/note="24 kDa protein; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="64 kDa protein"
'protein_id="AAC25118.1"
'db_xref="G1:3283086"
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product="65-kDa_protein"
protein_id="AAC25117.1"
db_xref="G1:3283079"
                                                                                                                                                                                                                                      oin(7983,8045. .9378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11311. .12972
/function="unknown"
/note="ORF 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9609. .11405
function="unknown"
                                                                                                                           gene="ORFla/b"
                                                                                                                                                                                                                                                                                 qene="CRF1a/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                    6096.
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                                                                                                                                                                                                                                                                                                                                                                                            rameshif
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                                                                                                                                                                                                                                      mat_peptide
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CYLAHAALCCALQKRTFREEDFYGWYTKRYFAKRLTEKLGPSALKHPWRGRQVSR
LFHCDVASAFSSPFYSLPFTGCVEEBAPETTSSLGHKALESVYERVSIHKDNILARS
VEXD.LDFKDEINSZLSKRRSVVTPFYWGEAVQSGLTRAYPQFNLSTHSVYSDHPAA
AGSRLLENETLASMAKSSFSDIGGCP-FHIKRGSTDYHVCR P. YDKKDAQRRVSRELQ
ARGJVENLSREQLVAGARNSVCPHTLGNCNVKSDVLJHVQYPDSSLBATSAMVLKE
SKYYLLMYPRGELLEBREARNDALGCDVVVDTRRDKYQYRGGSGYCHKLSNIKNI
MLTPAFTFSGNLFSVEMYENRYGVNYXKITRSAYSPETRGVKTLRYRRACTEVVQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PREDXTLKTELSGYDYIYLDAKFVSRVPDYVGNCSVVNSKTFEWWGYIKSSKSRVV
ISGYVIRBDYHIDLAGSCFAAVMLAVGVRRTTTEFLAKNLNYYTGASCFETIRFL
FRWSRRAYAEINRSFRKLMKSILSAGLDYFELDDNSLQHLLESYSEVRVSTAGNOG
EVDGNEENRVLTETIAAAAARKSILSAGLSSYPYOPRGGLRGGSRRGVBFLYN
VEEVGNLFFSVGDAVRFLVKVFKTFSDSPIFRVVRMFLDLAEAASPFVSVVSLCAWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVSASSWADDRIVESSVETEVINETUKRELIEMENAKULTKKEPEFELGASALAKTUV
RKAKVILEAYWEVWEESLLSDSGEYSAVEFCSSVVITULTNSGRLLPGFSPSAVITEV
LLDLATKISIEVLLKOISPUDSTASSALYRRVILSEILSNFRYMGEHGIFTKVFLLGF
LPVFVRKCVALCVPGDMATYAFELESVUDDLFFLGRSVVSIKNYLCVVAAGLVDSIVD
LRGGSSRETLSRLLDIFFLGEKXIKNFLAVFRKAKVVTRTSSSTDLSEDSYFSCDESKP
LRGGSSRFTLSRLLDIFPNFLKSSKLVIENACFSAYERIERNMALYFFPLNSSEERR
RLIRCAGDFDYLSDSAFDEDEMLRQAFEQYYSSDDESVTVDGKPTVLRSYLNVSRRFJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFFFPEEPKKDKAKGASLPTKDEGFITFGTLRFPLSETPKEEPRLPKFREVEIPVVKK
HAVPAVVSKPVRTFRPVATTGAEYVNARTQCSRRPRNHPILKSASYTFGFKKMPLORF
MKEKKDYYVKRSKVVSSCSVTKSPLEALTSILKNLPRYSYNSERLKFYDHFIGDDFEI
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ITACECVSQICCLRLIRLCWGTPACGLVRLFYITYSGTRVLSRVVVAVAVCPLLVRNE
LDGLSDGLTNMGVSVPRRLFVALRRALSAYSNSALRRKIFEFIFGNIHHPFDVAVIET
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FKJACRIPRLJFRLENFVAYEVERRJASKRLKTFIGLARJFDNFSLTSVVYLLJEYDS
VLNAFIDVELVJJNSGSVNVLPLVSKVRGSLTKLAEVIVGSGFASFLGRXCCRVSDWC
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EERPYEVTEPDIEHTSEDVVPIRSHSQPLSGGBCSYSEDREENBRANLLPHVSKIVSE
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ALFELSCKLREYYDQLKVANFNRQECLCDKDEDMFVLRAGGGVVSGRNSRLPLKHFKD
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APPGGGKTTTLIKVFCETFSKVNSLILTANKSSREEILAKVNRIVLDEGDTPLQTRDR
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AYRVYPTSFGGSTLDISVNPSTSDRSKCKASSAPYEVINSFLESVVPGTTSVDFGDVS
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MAMVMLERSFDLEKVAKVRSDVIAITEKGVRTYMSKREPSQLRALSSDLQKPLNLEEE
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RFKALFVSGDDSLIFSESPIRNSADAMCTELGFETKFLTPSVPYFCSKFFVMTGHOVF
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EAYFLTYDET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAFLNVSAVPSCAFAPAFAPHAGASPIVPDSFPCVPRYSDDISH
FRLTLSLDFSVPRPLFLNARVHLRASTDNPLPSLPLGFHAETFVLELNGSSAPFSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHIDFVVNRPFSVFPTEVLSVSSLRTPSRLFALLCDFFLYCSKPGPCVEIASFSTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLVSNCVAQIPTHAEMESIRFPTKTLPAGRLLQFHKRKYTKRPETLIIHESGLALKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGVTSKPNSRPITVKSASGEKYBAYEISRKDFERSRRRQQTPRVRSHKPRKINKAVE
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Submitted (31-MAR-1998) Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA Location/Qualifiers
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/gene="ORF1a/b"
/product="papain-like leader peptide"
                                                                                                                                                  organism="Beet yellows virus"
                                                                                                                                                                                                                                                                                                                                                                                 jcin(108. .7983,8345. .9381)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/db_xref="GI:3283077"
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/isolate="Californian"
                                                                                                                                                                                                                                                                 'db_xref="taxon:12161"
                                                                                                                                                                                                                                                                                                                                                 /gene="ORFla/b"
                                                                                                                                                                                                                                                                                                         .9381
                                                                                                                   .15468
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KGKDVVESTDEAVVSSSYLDYLSHCINLYETCNLSSNSGKKALYDEPLKYVIAYLETS
DLEYRSPSDNPLVAGVLYDWCFEYNTLKSTYLKNIESPDCFLSLYLPLLSEIFSWNWE
ORAPDVRLLPELDTARLLLKIPTINTLDSTFLYKNKLRYLESYFEDDSNELIKVKVDS
LLTRDNPELKLAQRWVGFPYTATTRKVYRDAYKKIPPLAGFTINWGVSFF
FDELDKKWFBYSVRRFCGSLSHEARSIFFKREGVGFPPITRLNVYXSYLNVDYYKH
VKRAGLTQDELTILSNIEFDVAEMCCEREVALQARRAQRGEKPFQGWKGVKNEVSPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETDELLGVIRERFKSELVITDEDFVKHLAFALIRAGNITTSTKVNYVGAYEYTIGGKK
FLVKDAWVFPLIKECMKKFNKPNPVRTFCATFEDAYIVIARSLPKLNLNRTIGKRGIP
SGYEFLGADFLTATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRLS"
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QKLLEGKRNKLRCFGTFQKDYISFAKEYRGRLPPTARANRHGLPAEDHYLAADFIST
STELTDLQQGRLLLARENATHTEFSSESPVTSLKQLGRGLATGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=ORF 2
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/txanslation="MLAPEGRGDLIHFTENTRDAMETFFNSYDLAEYSBVNPNKLNRK
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                                                                                                                                C2-AUG-1993
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                                                                                                                                                  two CRFs.
                                                                                                                                                                                                                                                                                                                                                                                                                          to genomic RNA
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                                                                                                                              VRL
                                                                                                                                                                                                                                                                                                                                                           protein
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Beet yellows virus coat protein gene, complete cds,
M59452
                                                                                                                                                                                                                                                                          DNA
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71
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                                                                                                                                                                                                                                                                                                                                                             coat
                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Beet yellows virus cDNA Location/Qualifiers
                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, closteroviridae; Closterovirus.

1 (bases 1 to 2724)
Brunstedt,J., Moseley,J. and Hull,R.
Nucleotide sequence of cDNA encoding the yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
                                             14234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA72953.1"
/db_xref="GI:323238"
      ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Beet yellows
/mol_type="genomic RNA"
/isolate="Broom's barn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="coat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:12161"
                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/label=ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/label=ORF 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ccdon_start=1
/label=ORF 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.64e-21
293.00
53.97%
37.57%
29.57%
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                                                                                                                                                                                       M59452.1 GI:323237
                                                                                                                                                                                                                                   Beet yellows virus
Beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1287
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1990)
                                                                                                                                                                                                                 coat protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scores:
      186
                                             14208
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                                                                                                                                                                                                                                                      CEGANISM
                                                                                                                              LOCUS
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ORIGIN
                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                  CCURNAL
                                                                                                                                                                                                             KEYWORDS
SOJRCE
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FEATURES
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                                                                                     RESULT 9
BYVVCPG
                                       Ω.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14031 TACCGAGGAAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT 14093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13731 AAACTACGGAGGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGATAAACTC 13790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13791 GGTCTCGCGTTAGGACTTTGTTGTACTCCTGTGCGACGATAGGTACTTCTAATAAAGTT 13850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !4091 CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAAGAGT 14150
                                                                                                                                                                                                                                                                                                                                 /codon start=1
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KILNRKVTFPESGGLUPGMYGRDGRCVSSEYLWFENVFVGAHGGTLPYCLNCELDX
SGGELEILTFSKNEVFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
)KLLEGKPNKLRCFCRTFQKDYISFAKEYRGRLPPIARANRHGLPAEDHYLAADFIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::i|i ||·:::|||:::
13911 CTCACGGCGAACTGAGGGTCCTTTCTGGACTTTTAGAGGAAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeuAsnGiyValAspLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProleuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                     STELTDLQQGRLLLARENATHTEFSSESPVTSLKQLGRGLATGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15468
71
31
85
2
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                   /function="replication enhancer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4426
                                                                                                        /codon_start=1
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                                                             function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3696 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNISIRVISSQILGIAV"
3472 c 3696 a
                                             14252. .14785
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295.00
53.97%
37.57%
29.77%
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Best Local Similarity:
Query Match:
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BASE CC ORIGIN

Score:

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/codon_start=1
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/db_xref="d1:318692"
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/translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGSSYLPGLLSRLSSVPFVEECLVLPDARAAVAGGCALYSACLRNDS PMLLVDCAAHN
LSISSKYCESIVCVPAGSPIPFTGVRTVNMTGSNASAVYSAALFEGDFVKCRLNKRIF
SOPALGDVGVFGSNTRTVELTLEINVSSVGTITFELVGFTGVKKLVGGNAAVDFSSY
OLGERVVADLHKHNSDKVKIIHALTYKPFQRKKLTDSDKALFLKRLSADYRREARKFS
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1937. .3598
                                                                                                                                                     /db_xref="SPTREMBL:Q65893"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEVAFGYDAEVLSNDSSVRGGFYRDLKRWIGCDEENVOOYLEKLKEHYKTELLKVAQS
SKSTVKLDOYSGTVPONATLPGLIATFVKALISTASEAFKCGCTGVICSVPANYNCLO
SKSTVKLDOYSGTVPONATLPGLIATFVKALISTASEAFKCGCTGVICSVPANYNCLO
NNTFVVRASGGOMGGROED TARAFWHLYKKAQLPVNYKIDISFLKKSLISKVSFLNF
PVVSEQNVKVDVLVNVSELAEVAAPFVHLXKAQLPVNYKIDISFLKKSLISKVSFLNF
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/tb_xref="SPTREMBL:Q5894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLASEGRODLIHFTENTRDAMETPFNSYDLAEYSEVNPNKLNRX
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FLUXDAMVPPLIKENGNENRPNPNTPCA-FEDAYIVIARGLEKELFNRTIGKK
FLUXDAMVPPLIKENGNERNRPNPNTPCA-FEDAYIVIARGLEKELFNRTIGKRGIF
SGYEFLGADPLTATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRELS
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STELTDLQQCRLLLARENATHTEFSSESPVTSLKQJGRGLATGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLNVDYYRHVKRAĞLTQDELTILSNI EFDVAEMCCERBVALQARRAQRREKPFQGWKĞ
VRNEVSPFARSSIRVKKSNESLLNI LWKDVGVRRQGRLNPLARKH"
           note="putative membrane-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="coat protein homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="coat protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5395. .5928
/note="orf8"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="orf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4878. .5411
/note="orf7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agranovsky, A.A., Koomin, E.Y., Boyko, V.P., Maiss, E., Lunina, N.A. and Atabekov, J.G.
2522
                                                                                                                                                                                                                                                                                                                          2106 GGTCTCGCGTTAGGACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAGTT 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACAAGTIGCGITGTITCTGCCGCACTITTCAGAAGGACTACATATCCTTCGCGAAGGAA 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2466 CGTCTGCTGTTGGCGCGGAAAACGCCACTCACACAGAGTTCTCG---TCTGAATCACCA
                                                                                                            LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlylle
                                                                                                                                                                            2046 AAACTACGGAAGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGACAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
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                                                                                                                                                                                                                                                       47 GluValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                              67 GinArgAlaAspSerAspValllePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X73475
X73475.1 GI:313689
X73475.1 GI:313689
protein, hear shock 70-related protein, membrane-binding protein.
Beet yellows virus
Beet yellows virus
Peet yellows virus
Closteroviridae, Closterovirus.
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Pflanzenvirologie, Biologische Bundesanstaldt, institut
Biochemie, Messeweg 11/12 D-3300 Braunschweig, FRG
Location/Qualifiers
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71. .235
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Cp Dp

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                     Agranovsky, A.A., Boyko, V.P., Karasev, A.V., Lunina, N.A., Kocnin, E.V. and Dolja, V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MDCVLRSYLLLAFGFLICLFLFCLVVFIWFVYKQILFRTTAQSN/
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7. Gen. Virol. 72 (Pt 1), 15-23 (1991)
911.6305
                                                                           beet yellows
                                                                                                                                                                                                                                                         Putative 65 kDa protein of beet yellows closterovirus is
homologue of HSP70 heat shock proteins
J. Mol. Biol. 217 (4), 603-610 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAY-1990) Agranovsky A.A., A.N. Belozersky Laboratory, Moskow State University, Moskow 119899, USSR 5 (bases 2678 to 6746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JUL-1990) Agranovsky A.A., A.N. Belozetsky Laboratory, Moskow State University, Moskow 119899, USSR
                                                                                                                                                                                     2 (bases 1 to 6746)
Agranovsky, A.A., Boyko, V.P., Karasev, A.V., Koonin, B.V.
                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 6746)
Renasing.S.A. and Maier,U.G.
Phylogeneric analysis of the stress-70 protein family
J. Moi. Evol. 39 (1), 80-86 (1994)
                                                                           Nucleotide sequence of the 3'-terminal half of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYDDAVLNSSELLGRIIPKILRGSRVEKLDV"
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         (bases 1 to 6746)
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Beet yellows virus genome 3'-proximal half, for capsid protein
HSP70 related protein, RNA-dependent RNA polymerase and ORFs.
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X53462.. GI:58878
Capsid protein; heat shock protein 70 homologue; RNA polymerase;
RNA-dependent RNA polymerase; unidentified reading frame.
Beet yellows virus
Beet yellows virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4357 AAACTACGGAAGAATTTCGAAGAGTGTTTAAAATTGAAAAGGGGTTCCGGAAGACAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 LeuleuSerAlaGluValGlulysMetLeuValGluLysGlyAlaProAsnGluGlyIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AsnLysLeuArgThrPheG_vArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4657 TACCGAGGAAGACTGCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT
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71
31
85
2
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Matches:
Conservative:
Mismatches:
Indels:
                   /db_xref="G1:313696"
/db_xref="SPTREMBL:Q65898"
                                                                                                                                                          1431 g 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4834 GTAACTAGTTTGAAACAGCTGGGTCGT 4860
protein id="CAA51863,1"
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                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                      4.64e-21
                                                                                                                                                                                                                                                                       293.00
53.97%
37.57%
29.57%
                                                                                                                                                        1267 C
                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                          1557
                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                      Pred. No.:
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89

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46

5235

5355

165

145

5472

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/mol type="genomic RNA"
/isolate="Ukrainian (BYV-U)"
/db xref="taxon:12161"
/db xref="taxon:12161"
/12 / 115, 1213, 1210, 124, 1313, 1311, 142, 143, 131, 1311, 142, 143, 156, 1510, 154, 1518, 1520, 169, 1615, 175"
1. .107
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                                                                                                                                                                                                                                                                                                                          106 AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5356 CACTACTTAGCCGCTGACTTCATATCGACGCACGGAACTCACTGACCTACAACATAAGT
      LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly1le
                                                                1996 AAACTTAGGAAGAACTTCGAAGAGTGTTTGAAATTAAAAGGGGTTCCGGAAGATAACCTC
                                                                                                                                   47 GluValValPheGlyLeuleuTyrAlaLeuAlaAlaArgThrThrSerProlysVal
                                                                                                                                                                                                555 GGAATCGCGTTAGGACTTTGTTTGTATTCCTGTGCTACGATAGGCCACTTCCAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                          86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5176 CTCACTCACGGGAATTGAATTCCTTTCTGGGGTCTCAAAAACTTTTGGAGGGAAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5416 CGTCTGCTGTTAGCGCGCGAAAACGCCACTCACACGGAATTCTCG---TCTGAATCACCG
                                                                                                                                                                                                                                                             67 GlnArgAlaAspSerAspVaillePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5236 AACAAATTGCGGTGTTTCTGCCGTACTTTCAGAAGGACTACATATCCTTGCGCAAGGAA
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Submitted (18-JUN-1993) A.A. Arganovsky, A.N. E
Moscow State University, 119899 Moscow, Russia
Related sequence: X53462.
Location/Qualifiers
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/organism="Beet yellows virus"
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Beet yellows virus
Viruses; SSRNA positive-strand
Closteroviridae; Closterovirus.
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Agranovsky, A.A.
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AUTHORS
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TITLE
JOURNAL
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SDTLNAFLEFYCRITGLAREDALREKYRKVKSVVLFHHSELLKFEVTENMFSYTELLK
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                                                                                                                                                                                                                                                                                                                   HVIDYLENSDLEYRSPEDNPLVAGILYDMCFFYYTLKSTYLGYISEROFFLSTYLEYL
SEVFSMYWERPAPDVRLLFELDAAELLLKVPTINMHDSTFLYKNKLRYLSYFEDDSN
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TKRFVSLIFKGKDLAESTDEAIVSSSYLDYLEHCLN.XFTCN.SSNSGKKSLYDEFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MGSAEPISAIATFENVSLADQTCLHGEDCOXLRRWFEECJKLKG
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KVARRKYFFFERVOLVGAFTGGKGVSSDYLMFERVFVGAHGGTLTYCLKTSELS
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Matches:
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protein_id="CAA37554.1"
db_xref="GI:58883"
db_xref="SPTREMBL:Q08531"
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/rote="ORF8"
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37.57%
28.86%
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Best Local Similarity:
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Pred. No.:
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ORIGIN
SGC
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us-09-613-486-15.rge

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RSFTESCWILSGYPCYYMYBESAALSACSRIKGATSPVLYYDFGGGTFDVSVISAL
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GGSSYLPGLLSRLSSIPFVDECLVLPDARAAVAGGCALYSACLRNDSPMLLVDCAAHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSISSKYCESIVCVPAGSPIPFTGVRTVNMTGSNASAVYSAALFEGDFVKCRLNKRIF
EQDVLGAVQVTGSARTVBFLTLEINVSSV3TISFSLVGFTGVKKLJGGNAAVDFSSY
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SYDDAVLNSSELLLGRIIPKILRGSRVEKLDV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MIAPEARGDIHFTENTRDAMETFPNSYDLAEYSEVNPNKLNRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative heat shock 90-related protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STELTDLQQSRLLLARENATHTEFSSESPVTSLKQLGRGLGTGR"
                                                                                                                                                                                                                'note="putative membrane-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="coat protein homolog"
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     045. .9393
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/codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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ARGLYENLSREQLVEAQARVSVCPHTIGNCVVKSDVLIMYQYYDASINEIASAMYLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKAKYI LEAVMEWPEGILSDGGEYSAYEFCSSVVITLITNSCRLLEPGFSPSAIITEV
LLDLATKI SIEVLLKQI SPADSTASSALYRRVLSEILSNFRTMGEHGI FTKVFLLGGF
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LRGGSSRFTLGRLLDPFPLKSSKLVI ENAGCFSAYER: ERNMKLYFFPLNSSEEBERA
RLIRCAGDFDYLSDSAFDEDEMIRQAFEQYYSSDDESVTYJGKFTVLRSSEERA
ETFCNGPKFFVKVSNYFKALYSRLLRVLPWVDRYLSDSPGLKGGNEKALLAKFFKTÇV
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ILTIDSYLMNNRGLTCKVLYLDECFWYHAGAAVACIEFTKCDSALLFGDSRQIRYGRC
SFLOTRVLSDINRFVDDESRYYGEVSYRCPWDVCAMLSTFYRWYSKOGSSM
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CLVSNCVAQIPTHAEMESIRFPTKTLPAGRFLOFHKRKYTKRPBTL:IHESGLALKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYLAHAALCCALQKRTFREEDFFVGMYPTKFVFAKRLTEKLGFSALKHPVRGRQVSRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVDCNEENRVLTEIIAEAADRKSIAQGLSGALSSVPTQPRGGLRGSSRRSGVSFLYNL
VEEVGNLFFSVGDAVRFLVKVFKTFSDSPIFRVVRMFLDLAEAASPFVSVVSLCAWLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITACECVSQICCLRLIRLCWGTPACGLVRLFYITYSSTRVLSRVVVAVAVCPLLVRNE
LOGGSDGLTHWGVSVPRRLFYALRRA.SASVSRBARRKIIE?FGNIHFPDVAVIET
NEVAPEPLSPEVDIVDCDFGSDSSVSSDFVASNPRGLHGGSRRSSNFJTSLVKVV
FKLARRIPRLLFRRNFVAXFVERRLASKRJKTFIGLARLFDNFSLTSVVYLLGETDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLNAFIDVELILLNSGSVNVLPLVSWVRGSLTKLAEAIVGSGFASFLGRMCCRVSDWC
SSSSNAGCNFMSPVRTKGKFVPPSSSGSTASMYERLEALESDIREHVLSTCRVGSDEE
EERPKEVTEPGIEHTSEDVVPIRSHSQPLSGGECSYSEDREENBRANLLPHVSKIVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRGLETARRNKRTLHGVSEFLNAINTSNEQPRPIIVDHSPESRALTNSVREFYYJQEL
ALFELSCKLREYYDQLKVANFNRQECLCDKDEDMFVLRAGQGGVVSGRNSRLPLKHFKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFKALFVSGDDSLIFSESPIRNSADAMCTELGFETKFLTPSVPVFCSKFFVNTGHDVF
FVPDPYKLLVKLGASKDBVDDEFLFEVFTSFRDLTKDLVDERVIELLTHLVHSKYGYE
SGDTYAALCAIHCIRSNFSSFKKLYPKVKGWVVHYGKLKFVLRKFANCFREKFDTAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAVDAVVSKPVRTFRPVATTGABYVNARNQCSRRPRNHPILIRSASYTFGFKKMPLGRF
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EVHPLRGGKLSVLLILPKGEAYCVVTAATPQYHAALTIARGDRPRVGELLQYRPGEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISGKVIHRDVHIJLKHSECFAAVMLAVGVRSRTTTEFLAKNLNYYTGDASCFETIRFL
FREWSRRAYAEINRSFRKLMKSILSAGLDYEFLJLDNSLQHLLEYSEVEVRVSIAÇNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALGUTSKPNSRPITVKSASGEKYEAYEISRKDFERSRRRQQTPRVRSHXPRKINKAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTFKLMVKRDAKVKLDSSCLVKHPPAONIMFHRKAVNAIPSPCFDEFKNRVITCTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIVEFTEMTNSTLASIAKEMLGSEHVYNVGEIDFSKFDKSQDAFIKSFERTLYSAFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEDLLDVWMQGEYTSNATTLDGQLSFSVDNQRKSGASNTWIGNSIETLGILSMFYYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFFPEEPKKOKRKRASLPTEDEGFITFGTLRFPLSETPKEEPRLPKFREVEIPVVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMGTQVFESGADNIVI RDSAPVNKSTDHEENLYSYESRNYNFTVCERFSGPQEFGQA
                                                                                                                                                                                                                                                     papin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="+1 ribosomal frameshift signal"
                                                                                                                                                                                                     /codon_start=i
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methyltransferase, RNA helicase"
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.7983,8645. .9393)
                                                                                          oin(108. .7983,8045. .9393)
gene="ORF1a/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108. .7983
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                                          /gene="ORFla/b"
|oin(108. .7983,
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SCTLNAFLEEYCRITGLAREDALRENGRKVKSVVLFHHSELLKFEVTENTHSSTELK
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Matches:
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Sequence 1 from Patent WO9428147.
A41914
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SGGELEILTFSKNEVLLKRW"
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          14768. .15301
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Best Local Similarity:
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Pred. No.:
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BYJ51931 10545 bp RNA linear VRL 05-APR-1999 elect yellow stunt virus helicase gene, partial cds; and RNA replicase, p30, p6, p66, p61, p25, coat protein, p18, and p22 genes, complete cds.
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    DNA
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70
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86
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      95
                                                             Bojsen, K. and Brunstedt, J.

DNA SEQUENCE COMPRISING AT LEAST TWO COAT
PATER: WO 9428147-A 1 08-DEC-1994;

SANDOZ AG (AT)

Other publication AU 7122694 541220.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
Viruses, ssRNA positive-strand viruses,
Closteroviridae, Closterovirus.
1 (bases 1 to 783)
                                                                                                                                                                                                                   Length:
Matches:
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ORGANISM

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KEYWORDS

VERSION SOURCE

us-09-613-486-15.rge

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QLVFKDKAVTEGAQWINSGSVSDYLVYCLQLYDNSKKKSNAGRTQLMESYVSFTRDFF

QHSDLYYRSPLDNPLATGVLYDLCIEHNVLRGSYLKMLDNRELFKOTYLEMIDDIFDY

SWELYAPDERLIFPIDPYEIIKEVPPMSVLOANVULSNKLYYLDSYLENNSITALEKK

IISILCRONGSTBARFRYGAKAGEAITVFKKLGISFPRITKLNAFSKYSYLNIDYF

KQANSLGLFPEKIILCNIAKDVDMMCAQRISSVKAKPIAQRNGEAINSAKIRTLFTN
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NLSIPNYVGESIVLVPAGAPVPFVOTRDINLASCVGSGSYSFVLFEDDRTKCFYNKKV
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FNGYNEQTADVCRILLGKSVQKTLRGARVEELSYRNIYEVQTLKI"
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VSRYGALEVSGSDDSI.IRSADEIANNSPEDIOLELGREFETKETTSVPYFCSRFLVPTGDK
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FEWGNIKLALSTIHCLRSNPLSFSKLFVKRTGWKVVYGKAKYILKKFLGYNIEPITTT
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VKQYDGNTGLLVYNGPHLILGGTIVRQFDILQGSCBNAYADLACPTSRFSFEVSDVL
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SSRGDPROFVLSSGEPEKKSVLRNRNEMCLFLLVLLLAGATIYVYPNLSRFGVS"
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FEFENCHVINGSFTCVHMMEBSAAALSTGGRDMSARNLLYDFGGGTFDVSVLSSL
NQTFVYASGGDMNLGGRDVDRAFKKLYGVANLPFDERAD'SSKIESISKIEVPFIT
TVKTKGGESKTVVVSRGLLAEVIVPFVDRIIKVMKRVFELYVKNMNLKAQDAKASLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
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                                                                                                                                                                                                                                                                                                                note="ORF2"
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                                                                                                                                                                                                                  FGDAWFVYKE"
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TLVSKFINLVNTENAFDEPRIIERAHDLASNSVREFYYLGELILIFFINKLNRYFSSELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHKKOR ILVLTANKSSQVEILKKINDSLKREHETKTKLLKFASKAERENYPSADSNVY
TIDSYLMÄHLGTKCDVLFVDECFMVHAGAVTAVSNTLVPRSVFFVGDSRQIHHIERNE
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TENSVDDVVASKRNYYLTFLÖSEKKELBKHLAKKGYRATWKTWHEGGOTTYRDVULV
TRYROPEDPROSFSPHINUATTRHTEGLTYAVLAARRUDNIAALCEANELUDFRLLTP
HSFGGSVLNIDVEPVYTDNSRCKASSAPINSINDFLEDVVPGSTSLNFGDTSAEMESQ
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SGNKLFHANTKFIAANSFLRSNSSYRNFIFENDSCRIRLYEAPPGGGKTHTLIASFVK
                                                                                                                                                                                                                                                                                                                                                    Screening of the closterovirus genome by degenerate primer-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF1b; similar to RdRp's of other closteroviruses;
the BYSV RdRp is presumably expressed via a +1 ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization of the beet yellow stunt virus coat protein gene Phytopathology 88 (10), 1040-1045 (1998) 4 (bases I to 10545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 10545)
Karasev, A.V., Nikolaeva, C.V., Lee, R.F., Wisler, G.C., Duffus, C.E.
and Dawson, R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Organization of the 3'-terminal half of beet yellow stunt virus genome and implications for the evolution of closteroviruses Virology 221 (1:, 199-207 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-MAR-1996) Alexander V. Karasev, University of Florida, Citrus Research and Education Center, 703 Experiment Station Road, Lake Alfred, Ft. 3850-2299, USA On Jun 25, 1996 this sequence version replaced gi:507953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 10545)
Karasev,A.V., Nikolaeva,O.V., Mushegian,A.R., Lee,R.F. and
Dawson,W.O.
                                                                                                                                                                                                                                               : (bases 2734 to 5576)
Karasev, A.V., Nikolaeva, O.V., Koonin, E.V., Gumpf, D.J. and
                                                                                                                                         Beet yellow stunt virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic RNA"
/specific_host="Sonchus oleraceus L."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Beet yellow stunt virus#
                                                                                                                                                                                                                                                                                                                                                                                        polymerase chain reaction

J. Gen. Virol. 75 (Pt 6), 1415-1422 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jocation/Qualifiers
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                                                                                                            Beet yellow stunt virus
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U51931 L20761
U51931.1 GI:1388128
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REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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Dises 1 to 672)

Roy,A., Ramachandran,P. and Brlansky,R.H.

Direct Submission

Submitted (12-AFR-2002) Plant Pathology, University of Florida, 700

Experiment Station Road, CRBC, Lake Alfred, FL 3385C, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /produčt="coat protein"
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ITYTEGGVEUDLSDEKLTEKRYPHNDEDROFTG
ITYTEGGVEUDLSDEKLTDVENSKGIGNRTNALRYMGRTNDALYLAFCRQNRNLSVG
GRPLDAGIPAGYHYLCADFLTGAGLTDLECAVYIQAKEQLLKKRGADEVVUNNRQLG
                                                                                                                                                                                                                                                                                                                                 9124 GACTTCGTCCAAACTAGCAACTTATTGAAAGAGCACGAACAGGCA---GTACTTCTGGAA 9180
3884 AAGACACCGTTAGTGAGCGCTAAGATAGATGCGGTCAACGTGACGATAACTTACGAAGAC 8943
                                                                                                                                                                                                                                               9064 CCGARTATCGCAAGAGCGAACAAACACGGTATTCCCCGCTGATTACTCGTATTTAGCAGCT 9123
                                                                                                                                                                                                                                                                                                                                                                                                                      9181 GGTAGAAACGCTGCTACAGCATCTTCCGGCACCACTAGGGAGTCTGCGGTCAACCTAAAA 9240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRL 02-APR-2003
                                       LeuLyslysvalLeuAspGlyCysAlaProLeuThrArgPheThrAsnlysleuArgThr 110
                                                                                                                                                                                                                                                                                           AspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGinSerArgLysMetPheAla 170
                                                                                                                        111 PheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHisLysLeu 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, A., Ramachandran, P. and Brlansky, R.H. Grouping and comparison of Indian citrus tristeza virus isolates based on coat protein gene sequences and restriction analysis
                                                                                                                                                   131 ProGinLeuAsnAlaAlaAlaGluLeuG.yileProAlaGluAspSerTyrLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                             171 SerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsnLeuArg
                                                                                 8944 ATTAAGAACTTGGTAAACTCCTTGACGTTGCTTAAGAACTATAAGAATAAACTCCGAGTÇ
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Viruses; 8sRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.
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61
27
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Matches:
Conservative:
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22548851
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/db_xref="taxon:12162"
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VERSION
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AUTHORS
TITLE
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SCURCE
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VMAGSGSDAIRKNEKNENLEPLSYMTTDLELMVRDIRÇLIRAEINKEFNCSSNQDVV
VMIINVINTHPSNSRERPVTFEQIQSFSMRGVIKTSLQNLSYKYKFEVTINYFKCNA
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VPMILNEDBELREVLGHKTEHKWIKALJEDTHHVARFLENRAVSYSEPKVGS
YSSSIDGRKYTWNDAKTFPOWILLASGHNKPWELRAFGASLEGMYLSYARLGPDAFGT
RSVGKRGAPSGSSYLGADFLISTCPLMSDHDRAVALSASRNALDRSAASGIDKKVVSL
                                                                                                                                                                                                                                                                                                                                                    /trānslation="WAGGNDEGSDDSSASQTWTAKDWIFAFENFARASATCLNGENK
KALFERENWYKTQDVTESSGIPTLAGATLYALANTSSSKIDIEDKTPPLVSAKIDAVN
VITITEDIKAFVNSTILLKAYKWKLRYFREEEVIAFVROYKHIDNIARAKHGI
PADYSYLAADFVQTSNILKEHEQAVLLEGRNAATASSGTTRESAVNLKYLGGSSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8704 AATTTGGCTCGCGCGCGCGCGACTTGTTTGAATGGTGAAACAAGAAGAAGTTGTTCGAG 8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8764 GAATTTTCTGTGAGAGTGAAGACTCAGGATGTCACTGAATCCGGCATTCCCACAACTTTG 8823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORF9; similar to the 20-kDa protein of CTV and the 21-kDa protein of BYV, two other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPhe
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/note="CP; CRF7; similar to coat proteins of other
closteroviruses"
                                                                                                                                 /note="transcription start site for coat protein subgenemic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /nore="similar to 3' UTR's of CTV and BYV"
2196 c 2497 g 2863 t
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="GI:1388136"
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/db_xref="G1:1388138"
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                                                                                                                                                                                                                                                                   evidence=experimental product="coat protein"
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function="unknown"
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product="p18"
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/product="p22"
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Best Local Si Query Match: DB:	Simi.	Similarity: 27.73% 13.17% 14	Mismatches: Indels: Gaps:	75 57 11	
JS-09-613-	436-1	US-09-613-486-15 (1-198) x AF501867 (1-672)	(1-672)		
çy Db	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	etGiuLeuMetSerAspSer) 	AsrLeuSerAsnLeuVal - \CTCTGATAGCG	1 MetGiuLeuMetSerAspSerAsnLeuSerAsnLeuVallleTnrAspAlaSerSerLeu 2	20
		snGlyValAspLysLysLeul	JeuSerAlaGluValGlu '::: :::::	AsnGlyValAspLysLysLeuSerAlaGluValGluLysMetLeuValGlnLysGly 4	46
3 %	0 1 4 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	darecenandarecenter.	GAMCASAGA IG=== SluGlyIleGluValVal	PheGlybeuLeuLyrAla 5	198 56
qg	199 A	::::::::::::::::::::::::::::::::::::::	::: Baggataaggacttccac	AAGTATCCTAACTTSCCTGACGAGGATAAGGACTTCCACATAGCTATGATSTTATATGT	258
		euAlaAlaArgThrThrSer		LeualaakaakgTbrThrSer	63
Db	259 T	TAGCGGTTAAGAGTTCATCG	rtgcaaagtgatgatgac	ACCACGGSCATAACATATACT 3	318
cy Jb	64 319 CC	ProLysValGlmi sell: 3GGAGGGTGTTGAAGTGGAT	rgalaasp ::: rg:c:gacaagcrirgo	ProlysvalginargalaaspSeraspvalilepheSer is:: ::: :	76 378
ć	77 A	snSerPheGlyGluArgAsn'	JalValValThrGluGly	77 AsnSerPheGiyGiuArgAsnValValThxGluGlyAspLeubysValLeuAsp 5	96
Db	379 A	AGGGTATTGGTAACCGT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		396
γĊ	97 G	lyCysAlaProieuThrArg	PheThrAsnLysLeuArg	GlyCysAlaProleuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr	9:1
QC	397 -		ACTAATGCCCTTCGA		432
Ċ	117 G	luAlaTyrValAspPheCys	lleAlaTyrLysHisLys	117 GluAlaryrValAspPheCyslleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAia 130	136
CC	433 G	CCCTTATTTAGCTTTCTGT	AGACAGAATCGCAAT	TIATERETTATGGTGGACGTCCG	681
Cy	137 A	laGluLeuGlyIleProAla:	SluAspSerTyrLeuAla	137 AlaGlubeuGly1leProAlaGluAspSerTyrbeuAlaAlaAspPhebeuGlyThrCys 156	951
qa	490 C	TAGATGCAGGGATTCCGGCT	GGATATCATTACCTATGI	GCAGATITCITGACCGGA	246
٥٨	157 P	roLysleuSerGluleuGln	SlnSerArgLysMetPhe	157 ProLysLeuSerGluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLys	176
qq	547 G	CIGGCIIGACIGAIITAGAA	rgrgcrgrgracaracaa		606
ζ	177 T	hrGluGlyGlyVal	ValAsnThrProValSer	177 ThrGluGlyGiyValVaiAsnThrProVaiSerAsnLeuArgGlnLeuGlyArg	194
Cp	607 A	agcgagggggggggggg	GTAGTTACT		657

Search completed: November 8, 2003, 30:59:54 Job time : 3533 secs

us-09-613-486-15.rng

Run on: 8

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Grapevine leafroll virus type 2 coat protein ORF6 product.
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                                                                                                                                                     AAV05870;
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AAV08870
                                                                                                                                                                                                                        Result
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| SIDSI | gogdata | geneseq | geneseq | encil | MA1999 | DAT: |
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                       frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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length: 200000000
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                                                                                         nucleic search,
                                                                                                                                   November
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Buchnera sp. genom
Erystpelothrix rhu
Erystpelothrix rhu
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Erystpelothrix rhu
Erystpelothrix rhu
Borella burgdorfe
Borella burgdorfe
Borella burgdorfe
Streptococcus poly
Genomic sequence o
                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faces
Grapevine leafrol:
Drosophila melanog
Drosophila melanog
Enterococcus faces
Enterococcus faces
Grapevine leafroll
Propionibacterium
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Rhizobium species
Nucleotide sequenc
Bacillus clausii g
                                                                                                          Grapevine leafroll
Sugar beet yellows
BYV coat protein c
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pSRQ800 fragment i
GLRAV-5 nucleotide
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Candida albicans e
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Probe #8204 for ge
Human brain expres
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Probe #7406 for ge
Probe #11068 used
                                                                                                                                                C. albicans BAX-as
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human galactokinas
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                                                                                                                                                                          Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orosophila melanoc
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                                                                                              Grapevine leafroil
and is derived by analysis of the total score distribution
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ABL02036
AAX13159
ABS98954
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ABK78469
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AAI42382
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AAQ87853
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640681
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X # X

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331 CTCACTAGGITCACTAAIAAACIIAGAACGITCGGICGIACTIICACTGAGGCIIACGIT 360
                                                                                                                           480
                                                                                           141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                            ATTCCAGCTGAAGATTCGTACTTAGCTGCAGATTTTCTGGGTACTTGCCCGAAGCTCTCT
                                                                                                                                                                                                                       181 ValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                          /product= polyprotein (protease, methyltransferase,
helicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLaV-2; closterovirus; grape; tobaccc; transgenic plant; disease resistance; birus resistance; beet yellows virus; tristeza virus; protease; methyltransferase; helicase; heat shock protein; coat protein; RNA polymerase; ss.
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product= RNA-dependent RNA polymerase
note= "Claim 29"
                                                                                                                                                                                                                                                                                                                                                                                                                  Grapevine leafroll virus type 2 (GRLaV-2) genome.
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note= "Claim 32"
1277..12932
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note= "Claim 41"
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/note= "Claim 43"
9551..11350
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product= coat protein
note= "Claim 38"
4180..14665
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product= undefined
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2844..13515
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product=
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                                                                                                                                                                                                                                                                                                            This is the nuclectide sequence of open reading frame ORF6 of grapevine leafroll virus type 2 (GLRaV-2) RNA (see AAV08874). It codes for a 22 bda coat protein (see AAV08864). It genome includes 9 open reading frames (see AAV08864-72) for a polyprotein, an RNA-dependent RNA polymerase, heat shock proteins, cat proteins of unknown function (see AAW3346-84). The polyprotein of produce antibodies useful for detecting These can be used to produce antibodies useful for detecting miscules can be used to produce antibodies useful for detecting molecules can be used to produce probes and primers for such molecules can be used to produce probes and primers for such colls, and to transform host cells (especially Agrobacterium tumefaciens, grape, citrus, beet or tobacco cells) and produce transgenic plants (claimed). They can be used to impart GRRaV-2 resistance to Vitis scion or roctstock cultivars or Nicotiana cultivars (claimed). Because extensive similarity exists between hisp?O-related sequence regions of GLRaV-2 and other clostercviruses, the DNA may also be used to impart beet yellows virus resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AsnGlyValAspLySJysLeuleuSerAlaGluValGluLySMetLeuValGlnLySJy
                                                                                                                                                                                                                                        to
                                                                                                                                                                                                                    Grapevine leafroll virus (type 2) proteins and polypeptides - and encoding DNA, useful e.g. to impart grapevine leafroll resistance grape and tobacco plants and detect grapevine leafroll virus
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                                                                                                                                                                                                                                                                                     Claim 38; Page 44; 151pp; English
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Best Local Similarity:
                                                                                                                                                                                      P-PSDB; AAW73482
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The nucleotide sequence of the novel gene encoding the sugar beet yellows virus (SBYV) capsid protein. The gene encodes a protein of 204 amino acids with mol. wt. 22.2 kD. The gene was obtained from reverse
                                                     13764 ACCACGTCTCCTAAGGTTCAGCGCGCAGATTCAGACGTTATATTTTCAAATAGTTTCGGA
                                                                                                               GluargasnValValValThrGluGlyAspleuLysLysValLeuAspGlyCysAlaFro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14064 GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGTCTAAAAACTGAAGGTGGA
                           61 ThrThrSerProLysValGinArgAlaAspSerAspValilePheSerAsnSerPheGly
                                                                                                                                                      13824 GAGAGGAATGTGGTAGTAACAGAGGGTGACCTTAAGAAGGTACTCGACGGGTGTGCGCCT
                                                                                                                                                                                                                                                                                          121 ASPPHECYSILEAlaTyrLySHiSLySLeuProGlnLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 GluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGLyGly
                                                                                                                                                                                                    1C1 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugar beet yellows virus cDNA fragment encoding capsid protein useful for production of virus-resistant transgenic plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 2 (GLRAV-2) has been sequenced and cloned from GLRAV-2 isolated from infected Vitis vinifers ov. Pinot Noir. About 83% costaed from infected Vitis vinifers ov. Pinot Noir. About 83% coftend from infected Vitis vinifers ov. Pinot Noir. About 83% coftinged from infected Vitis vinifers ov. Pinot Noir. About 83% coffirmed from several overlapping clones. The sequence in the cost protein gene region was determined and confirmed from several overlapping clones. The sequence of GLTAV-2 includes 9 open reading frames (see also AAV08864-72) encoding a polyprotein (see AAW71476) having papain-like proteins of GLTAV-2 includes 9 open reading frames (see also proteins of unknown function (see AAW71476, ABV1476) having papain-like proteins of unknown function (see AAW71476-84). These proteins can be used to produce antibodies, useful to detect GLRAV in samples e.g. by ELISA (claimed). The nucleic acid molecules can be used to produce probes and primers for such detection, and to transform host cells (especially Agrobacterium vitis, Agrobacterium tumefactens, grape, cittus, beet or tobacco cells) and produce transgenic plants (claimed). In particular, they can be used to impart GLRAV-2 resistance to vitis scion or rootstock cultivars or Nicotiana (claimed). Because extensive similarity exists between history variate between the DNA may also be used to impart beet yellows virus resistance to cittus scion color transform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AlabroAsnGluGly1leGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AsnGlyValAspLySLySLeuLeuSerAlaGluValGluLySMetLeuValGlnLySGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuValileThrAspAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                       Grapevine leafroll virus (type 2) proteins and polypeptides - and encoding DNA, useful e.g. to impart grapevine leafroll resistance to grape and tobacco plants and detect grapevine leafroll virus
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Aaw73482, Aaw73483, Aaw73484.
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15285..15500
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96 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GETCTCGCGTTAGAACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 GluValValPheGlyLeuLeuLeuTyrAlaleuAlaAlaArgThrThrSerProLysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAT42975-77 represent cDNA sequences encoding coat proteins from beet yellow virus (BYV) beet western yellow virus (BNYV) and beet necrotic yellow vein virus (BNYVV) respectively. These sequences are used in the recombinant DNA sequence of the invention. This comprises nucleotide sequences encoding the coat proteins of at least one luteovirus and at least one closterovirus. This recombinant DNA may be used to transform sugar beet for combatting viral infection. Other plants may also be transformed e.g. fruit such as mangoes, apples, pears, bananas, and field crops such as sunflower, wheat, barley, maize, and vegetables such as potatoes, carrots, cabbage and onion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA sequence comprising at least two coat protein genes - used to combat viruses in e.g. sugar beet
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Gaps:
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(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUMGEN VERW GES MBH.
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                        Beet yellow virus.
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       The fragment is useful for
                                                                                                                                                                                                                                                                                                                              SerAsnieuSerAsnieuVallieihrAspAlaSerSerieuAsn3iyValAspiysLys
                                                                                                                                                                                                                                                                                                                                                                                                        27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco mosaic virus; coat protein; beet yellow virus; BYV; beet western yellow virus; BWYV; beet necrotic yellow vein virus; BNYVV; luteovirus; closterovirus; sugar beet; fruit; mango; apple; pear; banana; field crop; sunflower; wheat; barley; maize; vegetable;
transcribed RNA isolated from purified SBYV. The fragment is the production of virus resistant transgenic plants by genetic engineering methods.

("pdated on 25-MAR-2003 to correct PN field.")

("pdated on 25-MAR-2003 to correct PF field.")
                                                                                                                 other
                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                             BP; 190 A; 155 C; 157 G; 186 T; C
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                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                             Sequence 688
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                                                                                                                                                   Alignment Scores:
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            CTCACTCACGGTGAACTGAGGTCTTTTCTGGACTCTCAGAAACTTTTGGAAAGGAAAGCCT 418
                                         AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla 125
                                                                                                                           TACCGAGGAAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT 538
                                                                                                                                                          SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                     539 CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAACAAGGT 598
                                                                                                                                                                                                                                   This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax resistant yeast or fungi, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasocropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bax, Bax-resistance, cytostatic; fungicide, immunosuppressive, virucide, vasotropic, vaccine; gene therapy, proliferative discreer; cancer; apoptosis, fungal; yeast, infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
                                                             TyriysHisLysLeuProGlnLeuAsnAlaAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                  ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
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                                                                                                                                                                                                                                                                                                                                                             ВР
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04-JAN-2001; 2001EP-0870002.
09-JAN-2001; 2001EP-0870003.
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preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polymorecotide associated with the Bax gene described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      919 CGTCTTTTGATTCAATCCGGTGTTTACGACCAAGTTGTTGAAAAATTCAAAGAAGCTGCT
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antisense molecules and antibodies are useful as medicaments or
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                          Arabidopsis thaliana DNA fragment SEQ ID NO: 48418
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28-APR-2999;
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05-MAY-1999;
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                               61 ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                               607 TACCAAGACTTTATTCTTAAGAGGCTTGAAATTTTCGTGCGGGAGCTTTACAGTTTAGGT
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834 CTICCAGGA---AGCAAATICCTTTACGCCGATGTCTATAAT-----CCTATGATGG 984
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                                                                                                                                                                                                                                                               LysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGlu 44
                                                                                                                                                                                                                                                                                                       ----GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the genomic sequence of Pyrococcus abyss; and P. abyss; proteins (see AAB96637.AAB96842). P. abyssi is a hypothic archaeon, which is isolated from deep-sea hydrotheral vents. The present sequence is a fragment of the genomic sequence of P. abyss. The 3 rend of this sequence overlaps with the 5' end of AAH41223. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysteuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleotide sequences isolated from Pyrococcus abyasi encode
proteins useful in industry -
                                                                                                                                                                                     /note= "This sequence overlaps with the 5' end
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Hyperthermophilic archaeon; hyperthermophilic protein;
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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                                                                                                   Location/Qualifiers
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Query Match:
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Querellou J,
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2179 ITTITIGAAAATATTACTTCAACTAATTCCAACGACAAGIGGATTAAAGAAATAAGCAAT 2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 AspleulystysValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRAV-5, grapevine leafroll virus, GLRAV infection, GLRAV coat protein,
GLRAV HSP70 homologue protein; viral gene mapping;
plant disease resistance; ds.
                                                                                                                                                                                                               ---SerAsrLeuValileThrAsp---
                                                                                                                                                                                                                                                                                                                             ------LysLeuSerRerLeuAsnGlyValAspLys-----LysLeuSerRla
                                                                                                                                                                                                                                                                                                                                                                                                                                           31 GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly---IleGluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 TTTATAGATTATTGTGTGAATGAAGAACATTTAGGGAATAAGGGAGCTATAAAATGTATT
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                                     "HSP70 homologous protein"
                                                                         Conservative:
Mismatches:
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hote= "Specifically claimed
1285..4094
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Query Match:
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138236 ACAGCCTTGGCAATAATGAAATTAGTGGAAGAGGGCGGATTAAGT-----TTGGATGAC 138289
                                                                           138290 -----CCCGTTGAGAAATTGGTTAATATAAAGCTTAGACCATTCGGAGAACCAGTGACC 138343
                                                                                                                 136
                                       CysalaProLeuThrArgPheThrAsn---LysLeuArgThrPheGlyArgThrPheThr 116
                                                                                                                 117 GlualaTyrvalAspPheCysLlealaTyrLysHisLysLeuProGlnLeuAsnAlaala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The 4.5 kb EcoRI fragment (AAT68648) of plasmid pSRQ800 includes a coding sequence for AbiE (AAW1788), a protein which, in Lactococcus lactis (L.l.), increases resistance to phages by aborting infection. pSRQ800 was isolated through examination of the phage resistance mechanism of L.l. subsp. lactis Wl. The total plasmid DNA of Wl was co-electroporated with shuttle vector pSA3 into phage-sensitive, plasmid-free L. lactis LM0230. Phage-resistant transformants were isolated and found to contain pSRQ800. The isolated DNA can be used to impart phage resistance to bacteria, esp. L.l., for use in the prodn. of fermented dairy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AbiE, phage abortive infection protein, phage resistance, pSRQ800, lactic acid bacterium, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated DNA encoding the AbiE protein of Lactococcus - for protecting strains used in production of fermented dairy products
                                                                                                                                                                                                                   138395 GAGGCCTTCATAGACGGAATGGTCGGTGGGGATAACTGGTTG 138436
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                                                                                                                                                                                         137 AlaGluleu----GlylleProAlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                       pSRQ800 fragment including coding sequence for AblE
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                                                                                                                                                                                                                                                                                                         AAT68648 standard; DNA; 4467 BP
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Matches:
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                                                                                                                                                                                                                                                           Buchnera sp. genomic DNA SEQ ID NO:1
                                                                                                                                                            BP.
                                                                                                                                                            ABA92787 standard; DNA; 640681
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                          Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2001
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                                                                                                                                                                                            ABA92787
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                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a grapevine leafroll virus (GLRaV-5) DNA sequence of the invention. The DNA sequence can be used in an expression construct. The construct is useful for providing resistance to GLRaV infection in a recombinant plant cell by transforming the plant cell with it, where transcription of the polynucleotide sequence interferes with a normal viral function such as movement, encapsidation or replication of viral RNA. The polynucleotide sequence is expressed as an antisense sequence and encodes a GLRaV coat protein, preferably a defective GLRaV coat protein or a GLRaV HSF70 homologue protein. The GLRaV-5 DNA is useful for the synthesis of GLRaV, as diagnostics and probes, for viral gene mapping and for induced plant disease resistance. It is also useful to detect and quantitate expression of GLRaV in plant tissue prior to use in vegetative propagation, by detecting the presence of GLRAV RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AspPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                     Novel grapevine leafroll virus polynucleotide useful as diagnostic and probe, for viral gene mapping and for induced plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3720 GGTAAGGAAGTGACAGTTGCCCATGATGAGATAAAGACAGCTCTAGACAATTCTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3780 TCTTTCGGTTACGAAACACTCCTAGACAATTTGGAAGAGCATTCACGGCAGCGATAGTG
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                                             /product= "duplicate coat protein"
/note= "Specifically claimed region"
"Specifically claimed region"
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Matches:
Conservative:
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Best Local Similarity:
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                                                                                                                                                            19-JUL-2000;
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The present invention describes a gene (I) derived from Buchnera sp. containing the DNA (a) or (b), (a) has a fully defined base pair sequence selected from a table of sequences found in the Buchnera sp. genemic DNA of ABA92787 given in the specification or is a DNA selected from complementary DNA sequences, and (b) is a DNA which hybridises with the DNA (a) and encodes a protein. Also described are: (I) a recombinant vector (II) containing (I); (2) a transformant (III) containing (II); (3) a genomic DNA of Buchnera sp. containing the sequence given in ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is a DNA containing a fully defined sequence given in ABA92786 or ABB92789 and (d) is a plasmid which hybridises with a DNA; and (5) a method for the preparation of a protein in which (III) is cultured and the expression protein of the objective protein is collected from the cresultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockroaches. The present sequence represents the specifically claimed Buchnera sp. genomic DNA sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435915 AAAAATCAACGTGGATCATTAAGCATTGATGACGAAGGTACTCCAGGTCAAAGAATATT 435856
                                                             -----AspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeu 162
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circular; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 AGATTAACGATTCCTGAACTTGATGAAGCATACGTTGATTTACTCGTGAATTACGAGGTG 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AACCGGCTCGAAAATATGATGGAAAAA 678
This sequence represents DNA encoding a 46.5 kD immunogenic fragment of the protective polypeptide antiqen (PPA) of the bacterium Erysipelothrix rhusiopathiae. This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous
                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ArgThrThrSerProLysValGlnArgAlaAspSerAspValilePheSerAsnSerPhe 79
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/*tag= b
/product= "Brysipelothrix rhusiopatniae 46.5 kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACACCGTATTTTAGTAAAATATGAAGGTAAAGTTAAA-----
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                                         435855 TTAATTGAAAATGGAATATTAAAAAAATATATGCAAGATAAACTTAATGCGGGTTTAATG 435796
                                                                                                                                                                    PheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys 123
                                                                                                                                                                                                                                                                                                                                 144 GluAspSerTyrieuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGin 163
                                                                                                                                                                                                                                                                                                                                                                                                                   164 GlnSerArgLysMetPheAlaSerWetTyrAlaLeuLysThrGluGlyGlyValValAsn 183
                                                                                      --GlyCysAlaProLeuThrArg 103
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                                                                                                                                                                                                                                                   124 llealaTyrLysHisLysLeuProGlnLeuAsnAlaAlaGluLeuGlyIleProAla
                                                                                                                                                                                                                                                                             !l recombinant protective polypeptide antigen useful as a vacaine
protecting livestock against Erysipelothrix rhusiopathiae
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/product= "Erysipelothrix rhusiopathiae 46.5 kD PPA
/product= fragment"
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(HGET ) HIGETA SHOYU KK.
(FUJI-): FUCITA GAKUEN.
  ValValThrGluGlyAspieurysLysValLeuAsp--
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P-PSDB; AAB14800.
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Alignment Scores:
                 RESULT 14
                                AAA50205
                                                            613 GCAGAAGTAAATTATTTACCTGAAGCGCATGAGGATTTCTTAGTTTCAGATTCAAGCGAG 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             673 TATAATGACAAACTAAATAATATCAACTTTGCTTTGGGTCTAGGGGTCAGCGAGTTTATT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                        The invention relates to a 46.5 kD immunogenic fragment (AAB148CO) of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix Thusiopathiae, and to DNA encoding it (AAA72113). This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous administration. The present sequence represents the coding sequence of DNA encoding the full-length PPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GlyGluArgAsrValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAla 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgThrThrSerProLysValGinArgAlaAspSerAspValllePreSerAsnSerPhe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 AGATTAACGATTCCTGAACTTGAAGATACGTTAGATTACTCGTGAATTACGAGGTG
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                                                                                                                                                                                                                                                      Novel recombinant protective polypeptide antigen useful as a vaccine for protecting livestock against Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GluAlaTyrValAspPheCysIleAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1881 BP; 719 A; 291 C; 384 G; 487 T; 0 other;
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Matches:
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fragment (AAB14800)"
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Gaps:
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                                                                                                                                                                                                                                                                                                               Example 1; Fig 2; 23pp; Japanese.
                                                                                                                                             (NORQ ) NORINSUSANSHO KACHIKU
(HGET ) HIGETA SHOYU KK.
(FUJI-) FUJITA GAKUEN.
                                                                                       99JP-0094004
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The present sequence is that of the Epa gene of strain Fujisawa of Erysipelctirix rhusiopathiae, the causative agent of erysipelas in antiger (see Arysipeloid in humans.) The gene encodes a protective antiger (see Arysipaloid in humans.) The gene encodes a protective antiger (spa A.I.) It was isolated from a genomic DNA library of strain Fujisawa by immunoscreening using E. rhusiopathiae convalescent polyseptide comprising residues 12-195 of the protein, especially a sidentified as a vaccine antiger. The N-terminal polypedide was shown to protect mice and pigs from a lethal challenge with E. rhusiopathiae. Vaccines containing immunogenic polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccines for protecting turkeys and pigs against Erysipelothrix rhusiopathiae infections comprising a polypeptide sequence from the N-terminal region of an erysipelas protective antigen -
                                                                                                                                                                                                                                Srysipelas protective antigen, Epa, SpaA.1; DNA vaccine, infection;
immuno-protective epitope; ds.
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                                                                                                                                                                         Erysipelothrix rhusiopathiae erysipelas protective antigen gene
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AAA50205 standard; DNA; 2040 BP
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/product= "Erysipelothrix rhusiopathiae full-length PPA"
487. 1692
                                                                                            60 ArgThrThrSerProLysValGlnArgAlaAspSerAspValllePheSerAsnSerPhe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujisawa strain; swine erysipelas; subunit vaccine;
                                                                                                                                      80 GlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAla
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(HGET ) HIGETA SHOYU KK.
(FUJI-) FUJITA GAKUEN.
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                                                                                                                                                                                                            The invention relates to a 46.5 kD immunogenic fragment (AAB14860) of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix rhusiopethiae, and to DNA encoding it (AAA72313). This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous administration. The present sequence represents
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Novel recombinant protective polypeptide antigen useful as a vaccine for protecting livestock against Erysipelothrix rhusiopathiae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2814 BP; 1048 A; 439 C; 558 G; 799 T; 0 cther;
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                                                                                                                                              Example 1; Fig 1A-1B; 23pp; Japanese.
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Job time: 383 secs
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Best Local Similarity:
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Sequence 3735, Ap Sequence 3735, Ap Sequence 3824, Ap Sequence 15086, A Sequence 17, Appli Sequence 7, Appli Sequence 17, Appli Sequence 15, Appli Sequence 15, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 31, Appli

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Run on:

```
GENERAL INFORMATION:

APPLICANT: Zhu, Hai-Ying
APPLICANT: Zhu, Hai-Ying
APPLICANT: Zhu, Hai-Ying
APPLICANT: Jing, Kai-Shu
APPLICANT: Gonsalves, Dennis
TITLE OF INVENTION: AND THEIR USES
TITLE OF INVENTION: AND THEIR USES
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devams & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
4 US-09-252-991A-3735

4 US-09-252-991A-3636

4 US-09-252-991A-3824

4 US-09-252-991A-18284

4 US-09-252-991A-16286

1 US-09-252-991A-16516

1 US-08-451-774A-7

2 US-08-451-774A-7

2 US-08-451-774A-7

5 PCT-US9-067-98-7

5 PCT-US9-067-98-7

5 US-08-08-12-1

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7 US-08-12-12-1

8 US-09-12-12-1

1 US-08-484-105-15-1

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1 US-08-948-155-50

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 US-09-103-840A-2

3 US-09-103-840A-1

US-09-422-869-1

US-09-813-817-3

US-09-978-197-3

US-09-978-197-3

US-09-521-0178-412

US-09-521-0178-412

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US-09-67-314-261

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US-09-522-991A-15531
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CLASSIFICATION:
PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09380983 Patent No. 6197948
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1491 4 US-
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l: /dgn2_6/ptodata/2/ina/5A_COMB.seq:*

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f: /cgn2_6/ptodata/2/ina/FUS_COMB.seq:*

f: /cgn2_6/ptodata/2/ina/Patenta/seq:*

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                                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-910-551B-1
US-09-252-991A-13503
US-09-252-991A-13503
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Result

Seguence 261, App Seguence 15531, A

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Sequence 3 Sequence 3 Sequence 4 Sequence 5 Sequence 5 Sequence 5

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AsrGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
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Patent No. 6197948
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Matches:
Conservative:
Mismatches:
Indels:
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                   991.00
100.00%
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Best Local Similarity:
Query Match:
DS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13884 CTCACTAGGTTCACTAATAAACTTAGAACGTTCGGTCGTACTTTCACTGAGGCTTACGTT
                                                 CUNTRY.

COUNTRY.

ZIP: 14603

ZIP: 14603

COMPUTER READABLE FORM:
MEDICY TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,933

FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-613-486-15 (1-196) x US-09-080-983-1 (1-15500)
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Matches:
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                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 60/C47,194
FILING DATE: 20-MAY-1997
ATTORNEY/AGENT INFORMATION.
NAME: Goldman, Michael L.
RECISTATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1631
TELECOMMUNICATION INFORMATION.
TELEPHONE: (716) 263-1304
Box 1051
Clinton Square, P.C.
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991.00
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nucleic acid
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              CITY: Rochester
STATE: New York
CCUNTRY: U.S.A.
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Best Local Similarity:
Query Match:
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Abortive Infection Protein
From Lactococcus
lactis, and Method of Use Thereof
                                                                                                                                                            APPLICANT: Sylvain Moineau, Barbara APPLICANT: Sylvain Moineau, Barbara APPLICANT: Sylvain Moineau, Barbara APPLICANT: Sylvain Moinear, Vedernthu, Jeffrey K. APPLICANT: Kondo
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: lactis, and Method of Use
NUMBER OF SQUENCES:
ADDRESSEE: Ian C. MoLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTRAILED STIEM: MS. LOSS (VERSION 4)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/56,907A
FILING DATE: December 1, 1995
CLASSIFICATION: 435
RICOR APPLICATION BATA:
APPLICATION NUMBER:
FILING DATE: MCLEOCHET NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-152
REFERENCE/DOCKET NUMBER: Quest 4.1-152
TELECAMINICATION INFORMATION:
TELEPAX: (517) 347-4103
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: N/A-
IDENTIFICATION METHOD: sequencing
OTHER INPORMATION: DNA encoding phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: phage abortive infection LOCATION: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                      Sequence 1, Application US/08565907A
Patent No. 5814499
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: IAN C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: Genomic DNA HYPOTHETICAL: NO
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IXMEDIATE SOURCE:
LIBRAY: genomic
CLONE: SMQ-20
POSITION IN GENOME: N/A
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4467
TYPE: Nuclectide
STRANDEDNESS: Single
TOPCLOGY: Sinear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
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FRAGMENT TYPE: N/A
CRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                            Sequence 1531, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMCKAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMCKAS FILLE REFERENCE: 107196.136
CURRENT PILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OP SEQ ID NOS: 33142
LENGTH: 2034
14004 ATTCCAGCTGANGATTCGTACTTAGCTGCAGATTTTCTGGGTACTTGCCGGANGCTCTCT 14363
                                                                                         14064 GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGCTCTAAAAACTGAAGGTGGA 14123
                                                      161 GluLeuGinGinSerArgLysMetPheAlaSerMetTyrAlaLeuJysThrGluGlyGly 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 GCCGGGGTAGAAGTCGGT------6TCGAAGGCTGT------655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 décedectedaarrectrisecerrescarescesecesecaatesreses 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 PheThrAshlysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AspLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsn 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 GluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSer 63
                                                                                                                                                               163 GlnGlnSerArgiysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 CAGGATGCGCGCCCC-----GGGGTGCGTTCGCGATAGAACCAGGCGGCGC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-613-486-15 (1-198) x US-09-252-991A-1531 (1-2034)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.00
43.04%
22.15%
9.68%
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Best Local Similarity:
Query Match:
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2179 TTTTTGAAAATATTACTTCAACTAATTCCAACGACAAGTGGATTAAAGAAATAAGCAAT 2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GluleuMetSerAspSerAsnLeu------SerAsnLeuVallleThrAsp--- 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AlaSerSerLeuAsnGlyValAspLys-----LysLeuLeuSerAla 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-613-486-15 (1-198) x US-08-910-551B-1 (1-4467)
                                                                                             PRICES APPLICATION 135
PRICES APPLICATION DATA APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeed
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-158
TELECOXMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: sequencing CTHER INFORMATION: DNA encoding phage OTHER INFORMATION: resistance PUSICATION INFORMATION: N/A US-08-910-551B-1
                            UMBER: US/08/910,551B
August 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: phage abortive infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus Lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NACE STREET TOPOLOGY: Linear NOLECULE TYPE: DESCRIPTION: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.00
41.89%
24.32%
8.58%
       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: WI
DEVELOPMENTAL STAGE: N
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CEJL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANELLE: N/A
IMMEDIATE SOURCE:
LIBRARY: genomic
CLONE: SMQ-20
POSITION IN GENOME: ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4467
TYPE: Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                      FILING DATE: AUCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
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                                                                                                                                                                                                                                                                                                                                                                                                  2059 GAATTITTAAATGAATTTAATCTAATCTGTCGAGAAAATAACTTAATTATTAATGATAAT 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:19 AAAACGAAAGTTGACAATTTCCCGTTTGTTGATAAATCGAGTAAATCGGATATTTTTCT 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2179 TITITIGAAATATTACTICAACTAATTCCAAGGAGAGAGTGGATTAAAGAAATAAGGAAT 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2395 GTTTTCGAAAAARTATTAGATTATCATTAAAAGATTCAGAGATTAAGTTATTTG 2454
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                                                                                                                                                                                                                                                                                                                                                   GluLeuMetSerAspSerAsnLeu------SerAsnLeuVallleThrAsp--- 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly---IleGluValVal
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APPLICANT: Sylvain Moineau, Barbara
APPLICANT: Shenzer R. Vedamuthu, Jeffrey K.
APPLICANT: Exember R. Vedamuthu, Jeffrey K.
APPLICANT: Acado
TILLE OF INVENTION: DNA Encoding Phage
TILLE OF INVENTION: Acceptive Infection Protein
TILLE OF INVENTION: Rom Lactococcus
TILLE OF INVENTION: lactis, and Method of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                            4467
36
26
46
40
                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                               JS-09-613-486-15 (1-198) x JS-08-565-907A-1 (1-4467)
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OPERATING SYSTEM: MS-DGS (version
SOFTWARE: Wordperfect 5:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ThrPheGlyArgThrPheThrGlu 117
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MEDIUM TYPE: 160 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08910551B
Patent No. 5910571
     resistance
N: N/A
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2190 Commons Parkway
                                                                                                                         0.466
85.00
41.89%
24.32%
8.58%
) OTHER INFORMATION: res

; PUBLICATION INFORMATION:

GS-08-565-907A-1
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: USA
                                                                                                                                                 Score:
Percent Similarity:
Best Local Similarity:
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STREET: 2190 (
CITY: Okemos
STATE: Michiga
                                                                                                  Alignment Scores:
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                                                                                                                               Pred. No.:
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Sequence 13408, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2299 TTCCCAGTTATA-------ACAAATACATTGAACAAAAAAAGTA 2337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 AspleuLysLysValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SerAsnLeuVallleThrAsp---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3. GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly---IleGluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2239 TTTATAGATTATTGTGTGAATGAAGAACATTTAGGGAATAAGGGAGCTATAAAATGTATT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                          NAME/KEY: phage abortive infection LOCATION: N/A LDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA encoding phage OTHER INFORMATION: resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2455 ACTITICALAMIATATICA 2478
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                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION: N/A
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                                                                                                                                                            ORGANELLE: N/A
IMMEDIATE SOURCE:
LIBRARY: genomic
CLONE: SMQ-20
POSITION IN GENOME: N/A
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.466
85.00
41.89%
24.32%
8.58%
                             INDIVIDUAL ISOLATE: W:
DEVELCPMENTAL STAGE: 1
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CELL LINE: N/A
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Query Match:
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Pred. No.:
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2239 TITAINGAITAITGIGIGAAIGAAGAACAITIAGGGAAIAAGGGAGCIAIAAAAIGIAIT 2298
                                                                                              ------ACAAATACATTGAAACAAAAAAAGTA 2337
                                                                                                                                                                   2395 GTTTTCGAAAAATATTÄÄÄTTTATCATTAAAAGATTCAAGATTAÄCTÄÄTÄÄGTTTTTG 2454
                                                                                                                                                                                                                       90 AspLeuLysLysValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                             50 PheGlybeuLeuLeuTyrAlabeuAlaAlahrgThrThrSerProbysValGlnArgAla 69
                                                                                                                                     70 AspSerAspValilePheSerAsnSerPheGlyGluArgAsnValValValThrGluGly 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sylvain Moineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenbergh,
APPLICANT: Generaer R. Vedamuthu, Jeffrey K.
APPLICANT: Kondo
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: Iactis, and Method of Use Thereof
                                                                                                                                                                                                                                                                                                                                                      2455 ACTTECTTTGAAAATATTAATGAA 2478
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OPERATING SYSTEM: MS-DOS (version
SOFTWARE: wordperfect 5.2
CURRENT APPLICATION DATA:
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTONNEY/AGGNT INFORMATION:
NAME: 1an C. McLeod
REGISTRATION NUMBER: 20,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 KD storage
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08909425A
Patent No. 5928688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (517) 347-4106
TELEFAX: (517) 347-4103
TELEX: No. 59266896
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA
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Linear
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. MC
                                                                                         2299 TTCCCAGTTATA-
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Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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ANTI-SENSE: NO
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1999-02-18

CURRENT FILING DATE:

us-09-613-486-15.rni

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; TYPE: DNA ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-13408

0.389 81.00 41.79% 22.39% 8.17%

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:

DB:

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Sequence 13350, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33:42
SEQ ID NO 13950
LENGTH: 2433
                                                                                                                                                                                                               17 AlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeu 36
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                      Matches:
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8.17%
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Percent Similarity:
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Cuery Match:
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Best Local Similarity:
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Pred. No.:
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US-09-1252-991A-13503
Sequence 13503, Application US/09252991A
Sequence 13503, Application US/09252991A
Sequence 13503, Application US/09252991A
Sequence 13503, Application Normalian Sequence 13512
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS
TITLE OF INVENTION: NUMBER: US 6.074,788
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-07-27
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Matches:
Conservative:
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               PRIOR APPLICATION NUMBER: US 60/674,788 PRIOR FLILMG DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 13408 LENGTH: 1743
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117 GluAlaTyr----

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TYPE: DNA ORGANISM: Pseudomonas aeruginosa

LENGTH: 2199

Alignment Scores:

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Best Local Similarity: 20.98% Mismatches: 60 Query Match: 7.97% Indels: 62 D5: 2	15 (1-198) x US-38-770-544-15 (1-1434)	32 ValGluLysMetLeuValGlnLysGlyAlaProAssGluGlylleGlu 47	Db 940 CTRCGCAGACTCGTTCTTTCGAAAGGCGGGGGTCAACACCACGAGATATGGGGAATATG 999 Oy 48 ValyalPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGln 67	Db 1000 ATAGTGGCCATGATACAACTTTTCGTACTCTACTGTAAAGAATATAAGCGTCAAA 1059 Qy 68ArgAlaAspSerAspValllePheSerAsnSerPheGlyGluArgAsnVal 84	1066 GACGGGTATAGGCTGGAGACCGAATTAGGTCAAAAGAGAGTC 1	Oy 85 ValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100	(y) 101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120	221 AspPteCys1leAlaTyrLysHisUysLeuProGlnLeuAsnAlaAlaAlaGluLeuGly 220 AspPteCys1leAlaTyrLysHisUysLeuProGlnLeuAsnAlaAlaAlaAlaGluLeuGly 2210 Actroatematatatatatatatatatatatatatatatatatat	141	1267 GTCCCGAAGAGGTTCACTCCGTACTCGACTTCGACTTACTGGATAATTAC	DD 1327 CCGCGGACGTGTTGAAGCCTAACGA 1353	Cy 169 PheAlaSerWetTyrAlaLeuLysThrGluGlyGlyValValAsmThrPrcValSerAsn 188	189 LeukrgGlnteugly 193	1387	RESCLT 1: US-09-579-15 US/09579259 : Sequence 15. Application US/09579259	Patent	APPLICANT: Gonsalves, Donnis Ling, Kai-Shu TITLE OF INVENTION: GRAPEVINE LEAFROLL	CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LiP STREET: Clinton Square, P.O. Box 1051			COMPUTER: IBM PC Compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.30	
Qy 37 ValGlnuysGlyAlaPrcAsnSluGlyIleGluValValPheGlyLeuLeuLeuTyrAla 56	57 LeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSer 	2196AACGAGCTGATCAAGGTCACCAAGGCCCCCGGCCTTCTACCAG 2	Oy	Oy 117 GlualaTyrValAspPheCyslleAlaTyrLysHis 128	129 JysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyllePro 142	Db 2028 CGCATCGCCCTGGACAATCCCGGCGTGCAGCTCGGCCTGCCG 1987 RESULT 10	US-08-770-544-15 ; Sequence 15, Application US/08770544 ; Patent No. 5907085 GEVERB, INFORMATION:	APPLICANT: Gonsalves, Dennis APPLICANT: Ling, Kai-Shu TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND TITLE OF INVENTION: THEIR 1988	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: NIXON,	STREET: Clinton Square, P.O. CITY: Rochester CTATE.	SIATE NEW TOTAL COUNTRY: U.S.A.	., COMPUTER REAGRANDE FORM: , MEDIUM TYPE: Floppy disk , COMPUTER: LEM PC compatible OPERATING SYSTEM: PC-FOS/MS-FOS	SOFTWARE: Patentic Release #1.3, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/770,544					; INFORMATION FOR SEQ ID NO: 15: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1434 base pairs	TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin	, MOLECULE TYPE: CDNA US-08-770-544-15	Alignment Scores: 0.543 Length: 1434 Score: 79.00 Matches: 43 Percent Similarity: 40.40 Concernation: 40.40	

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Length:
Matches;
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                                                                                                                Sequence 1, Application US/09214808A Patent No. 6475793 GENERAL INFORMATION:
                                          1401
  LeuArgGlnLeuGly 193
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79.00
38.27%
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7.97%
                            1387 TTAAGGCGTAAAGGT
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CRGANISM: Rhizobium
US-09-214-808-1
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Query Match:
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Pred. No.:
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Matches:
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                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMINACATION INFORMATION:
TELEPHONE: (716) 263-1804
TELEPHONE: (716) 263-1600
APPLICATION NUMBER: US/09/579,259
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID KC: 15:
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                FILING DATE: 25-May-2000 CLASSIFICATION: <UNKnown>
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SEQUENCE CHARACTERISTICS:
LENGTH: 1434 base pairs
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STRANDEDNESS: single
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40.49%
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314743 ---GGAACGGCAAAAAACTTCTGGCACGGGGTATTCATGAAGCTGCCAGACGTTCCGGC 314799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315034 ATCCTGGCATCGACGCGGCCGCTTCCTGAGTTGGGCTCGAGCGGGGCAGCTG---ATACCT 315090
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APPLICANT: Rosenthal, Andre
APPLICANT: Resenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Preiberg, Christoph
APPLICANT: Preiberg, Christoph
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPOGG CURRENT APPLICATION NUMBER: US/09/214,838A
CURRENT APPLICATION NUMBER: US/09/214,838A
FRIOR RILING DATE: 1999-66-22
FRIOR RELING DATE: 1999-67-10
NUMBER OF SEQ ID NOS: 1
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CS-09-252-991A-3636/C
Sequence 3636, Application US/C9252991A
Sequence 3636, Application US/C9252991A
Partent INFORMATION:
APPLICAVE: Marc J. Rubenfield et al.
APPLICAVE: Marc J. Rubenfield et al.
TITLE OF INVENTION: WCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US 60/074,788
PRIOR APPLICATION WUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NEXAMBLE OF SEQ ID NOS: 33142
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                                                             754 GICCAICCITCGCAACTGGGTTCGCGTGCCCTGGCCGAGAACATCTCGGCGTTGCTGACC 813
                                                                                                                          Glu-----LeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                        143 AlaGluAspSerTyrLeuAlaAlaAspPheLeu-----GlyThrCysProLysLeuSer 160
                                                                                                                                                                          814 GASITCCACCTSCCGCCCAGTTCGGTGATSTTCGAGATC--------ACOGAG 858
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                                                                                                                                                                                                                          179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet
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Matches:
Conservative:
Mismatches:
Indels:
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77.50
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25.00%
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Best Local Similarity:
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APPLICANT: Marc J. Rubenfleid et al.
APPLICANT: Marc J. Rubenfleid et al.
APPLICANT: Marc J. Rubenfleid et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECUENCES RELATING TO PSEUDOMCNAS TITLE OF INVENTION: ABRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENKCE: 107.96.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1233
315091 GCTCTTGAGTCGCGTCTCGCGCCGGGTCACGTCTTTCTTCCCCCTCTATGCGATCGCCTC 315150
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                                                                                315151 GAAGATCTTCCACTCCTAGCTGAACACTTCCTACAAGGGCTCCGAAAG 315198
                                             154 GlyThrCysProLysLeuSerGlu-----LeuGlnGlnSerArglys
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Matches:
Conservative:
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                                                                                                                                                                                          Sequence 3735, Application US/09252991A
Patent No. 6551795
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7 ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3735
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Pred. No.:
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Search completed: November 8, 2003, 01:42:06
Job time : 140 secs
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

SEQ ID NO 3824

LENGTH: 4884
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                                                                                                                                                                                                                                                                                         179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 GTGATCCTCAGCAGCAGGTGGATCCCATCCTGCGCCAGGCCACCATTTCGATGATCGAG 262
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                                                                                                                                                                                                                  Glu----LeuGlnGlnSerArgiysMetPheAlaSerWetTyrAlaLeuLysThrGlu 178
                                                                                                                                                                                                                                                 519 GAGTICCACCIGCCGCCCAGIICGGIGAIGTICGAGAIC------ACCGAG 475
                                                                       123 CysīleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro 142
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                                684 ACCTACAACCTGGTCGACAAGCTGTTCTGGCAACTGTTCAGCCAGGGG------
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PheGlyArgThrPheThrGluAlaTyrValAspPhe
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Sequence 3824, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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Sequence 1, Appliant of the control 
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13 US-09-974-301-1589
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDSMI
APPLICANT: WATANABE, HIDSMI
APPLICANT: WATANABE, HIDSMI
APPLICANT: WASAHIRA
APPLICANT: GENERAL, YOSHIYUKI
ITLE OF INVENTION: GENOME DNA OF BACTERIAL SYM
FILE REFERENCE: 08136/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRICR FILING DATE: 2000-04-07
NUMBER: PATENTING DANS: 7
SOFTWARE: PATENTIN ON NOWER: JENOME STANDARD STA
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Patent No. US20020127687A1
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ORGANISM: Buchnera
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(c) 1993 - 2003 Compugen Ltd
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Publication No. US20030148390A1
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
APPLICANT: LING, KAI-SHU
TILLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES
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Matches:
Conservative:
Mismatches:
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  SCFTWARE: FastSEQ for Windows Version 4.18 SEQ ID NO 6624
LENGTH: 1356
TYPE: DNA GRGANISM: Enterococcus faecalis FARTURE: NAME/KEY: CDS
LOCATION: (1)...(1356)
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APPLICANT: CASSIDEN, KARIL.
APPLICANT: CASSING, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tradic's, John D.
APPLICANT: Tradic's, John D.
APPLICANT: Tradic's, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 1000-10-21
PRIOR PPLICATION NUMBER: 60/101, 078
PRIOR PPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/245, 598
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245, 598
PRIOR PPLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255, 931
PRIOR FILING DATE: 2000-11-27
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Patent No. US20020061569Al
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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            CURRENT APPLICATION NUMBER: US/10/138,842A
CURRENT FILING DATE: 2002-05-03
PRIOR PAPLICATION NUMBER: US 09/579,259
PRIOR PAPLICATION NUMBER: US 09/224,898
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: US 06/009,008
PRIOR FILING DATE: 1995-12-21
PRIOR FILING DATE: 1995-12-21
PRIOR FILING DATE: 1995-12-21
SOFTWARE: FASTSEQ for Windows Version 4.0
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; ORGANISM: Grapevine Leafroll Virus
US-10-138-842A-15
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FILE REFERENCE: 07678/025036
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            Doyle Li.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1434
43
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62
                                                                                           APPLICANT: D. DOCUMENTO TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                            Hargrave, Devans & nare, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    060 GACGGSTATAGGGTGGAGACCGAATTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              924 TIGCCGATAACGGAAGCICTACAGATAAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/039,112
FILING DATE: 31-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DCS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PAPLICATION UNMBER: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave
STREET: Clinton Square, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Michael L.
US-16-039-112-15

Sequence 15, Application US/10039112

Publication No. US2003C198942A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                    APPLICANT: Gonsalves, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                              ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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40.49%
20.98%
7.97%
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ULE TYPE: cDNA
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                      CITY: Rochester
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Query Match:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 222: US-09-070-927A-222	Alignment Scores: 26 Length: 11597 Score: 79.C0 Matches: 53 Percent Similarity: 36.53 Conservative: 27 Best Local Similarity: 24.20 Mismatches: 73 Query Match: 10.97 Indels: 66 DB: 12	US-09-613-486-15 (1-198) x US-09-070-927A-222 (1-11597) US-09-613-486-15 (1-198) x US-09-070-927A-222 (1-11597) US-08-613-486-15 (1-198) x US-09-070-927A-222 (1-11597) US-08-613-486-15 (1-198) x US-09-070-927A-222 (1-11597) US-08-613-486-15 (1-198) x US-08-08-08-08-08-08-08-08-08-08-08-08-08-	FILE REFERENCE: CARPO068 CURRENT APPLICATION NUMBER: US/09/939,964 CURRENT FILING DATE: 2001-08-27 PRIOR APPLICATION NUMBER: 09/214,808 PRIOR FILING DATE: 1999-06-22
::::	Oy 101 LeuThrArgPheThrAsniysLeuArgThrPheGlyArgThrPheThrGluAlaTyzVal 120		TERISTIC 597 base eic acid SS: doub linear

us-09-613-486-15.rnpb

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Page

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Sequence 6808, Application US/10032585
Publication No. US2030180353A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
ITILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TITCIGCGGGAIGAIGACACAGIGAAAGIAAGCCGGICCATTAAAGAATTAAGCAATAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 TyrLeuAlaAlaAspPhe-LeuGlyThrCysProLysLeuSerGluLeuGlnGlnSrAr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 LewArgThrPheGlyArgThrPheThrGluAlaTyrvalAspPheCys:leAlaTyrLys 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 HislysLeuProGinLeuAsnAlaAlaAlaGlu---LeuGlyIleProAlaGluAspSer 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 ValGlnLysGlyAlaProAsnGluGlyIleGluVal-----ValPheGlyLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 TyralaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSer---AspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 ATTGGTTTA--------ATTAAGTCTGTCGACAAATTTGACCTT
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: 665
TYPE: DA
TYPE: DA
ORGANISM: Bacillus clausi:
FEATURE:
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77.50
40.84%
23.56%
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                               1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValValValThrGlu---G.yAspleuLyslysValleuAspGlyCysAlaProleuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 GluGiyileGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSer
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Batent No. US20020146721A;
GENERAL NIFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                               Conservative:
Xismatches:
Indels:
                                                                                                                                                                                                                                                                                                         US-09-613-486-15 (1-198) x US-09-939-964-1 (1-536165)
                                                                                                                                                                           Length:
Matches:
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                     2.17e+34
79.00
38.27%
26.02%
                   SOFTWARE: Patentin Ver. 2.; SEQ ID NO 1; LENGTH: 536165; TYPE: DNA 7, ORGANISM: Rhizobium US-09-939-964-1
   NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                       Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AlaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAla 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TyrValAspPheCysileAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGlu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 LeuGlylleProAlaGluAspSerTyrLeuAlaAspPheLeuGlyThrCysProLys 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 LeuSerGlubeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        799 ------CAATTAGAAACTAAATATAATGATTTGTTTAAGGCATTG------ 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874 AACGAGAACACCGATGACACCATTCATACCAGTAAAGTAAAAGTTTTATTGAATATTGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                934 -------AATAATGTTCAAGGTAAAATGTTACTTTACAAGAGAA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ThrSerProLysValGlnArgAlaAspSerAspVaillePheSerAsnSerPheGlyGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 GlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                        2 GlubeuMetSerAspSerAsrbeuSerAsnbeuVallleThrAspAlaSerSerbeuAsn 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluVal 197
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 10:82-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 6608
LENGTH: 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-156-761-4239
US-10-156-761-4239
; Sequence 4239, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMERA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1209)..(1209)
OTHER INFORMATION: n=g, a, t or
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77.00
35.68%
19.60%
7.77%
                                                                                                                       TYPE: DNA ORGANISM: Candida albicans
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Horne, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Loyue
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPRENCE: 4921-5028-W0
CURRANT PELICATION NUMBER: US/09/880,107
CURRANT FILING DATE: 2001-66-1
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/217,379
PRIOR APPLICATION NUMBER: US 60/237,054
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHORYWI, YOSHIYUKI
APPLICANT: HATYORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PLILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 4239
LENGTH: 1068
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.34
76.50
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3C.09$
7.72$
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; LOCATION: (1)..(1068)
US-10-156-761-4239
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Best Local Similarity:
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Pred. No.:
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DB:
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115 .68 125 945

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7245 CTGCAGAGACGACTATGAGGTSAGCTGCCCAGAGCTGGACCAGCTGGAGGTGGGGCT 7304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 rLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 SerAsmSerPheGlyGluArgAsmValValValThrGluGlyAspLeuLysLysValLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AlaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValllePhe 75
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                                                                                                                                                                                  OTHER INFORMATION: Genbank Accession No. US20020142981A1 176927
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Matches:
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APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, HIROSHI
APPLICANT: SHIRA, HAROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANTON: WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT FILING DATE: 2002-05-29
PRIOR PLICATION NUMBER: JP 2001-204099
PRIOR PLILNG DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10156761 Publication No. US20033119018A1 GENERAL INFORMATION:
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76.50
38.06
23.88
7.72
NUMBER OF SEQ ID NOS: 3950
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                                         SOFTWARE: Patentin Ver.
SEQ ID NO 2228
LENGTH: 8095
                                                                                                                TYPE: DNA CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                              Pred. No.:
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RESULT 12

US-39-864-761-8204/c

US-39-864-761-8204/c

US-39-864-761-8204/c

Sequence 8204, Application US/09864761

Sequence 8204, Application US/09864761

Septembre 10. US20020049763A1

SEDERAL INFORMATION:
APPLICANT: Bank, Darion G.
APPLICANT: Bank, Sharion G.
APPLICANT: Bank, Darion G.
APPLICANT: Chen, Wensheng

IITLE OF INVENTION: HUMBER 10.29/864.761

CTREAT APPLICANTION: HUMBER: US 09/864.761

CTREAT APPLICANTION NUMBER: US 00/10.23

SPRIOR APPLICANTION NUMBER: US 00/10.24

PRIOR APPLICANTION NUMBER: US 00/20.466

PRIOR APPLICANTION NUMBER: US 09/632.366

PRIOR APPLICANTION NUMBER: US 09/632.366

PRIOR APPLICANTION NUMBER: US 09/632.366

PRIOR APPLICANTION NUMBER: US 00/10.04

PRIOR APPLICANTION NUMBER: US 00/10.04

PRIOR APPLICANTION NUMBER: POT/USO1/00666

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                                                                                                                                                                                                                                                                                                                                                                                US-09-613-486-15 (1-198) x US-10-156-761-1 (1-9025608)
                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                         g, other or unknown
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76.50
40.71%
30.09%
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NAME/KEY: misc feature ; LCCATION: (4187715) ; OTHER INFORMATION: a, t) US-10-156-761-:
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Best Local Similarity:
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Pred. No.:
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Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynuciectides and Polypeptides
NUMBER OF SQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CCUNTRY: USA
                                                                    ---LeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArg 166
                                                                                                                                        167 LysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProVal i86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SerAlaGluValGlu 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                         126 TCCTGGCTTTCACAACTGCGCCTCCTGAAACTGATG 91
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-MAY-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION ADATA:

APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/066,039
FILING DATE: 1997-01-14
ATTORNEY/AGENT INFORMATION:
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Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 238
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REGISTRATION NUMBER: 40,332
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 238, Application US/09070927A
Patent No. US20020120116A1
SENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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SEQUENCE CHARACTERISTICS:
LENGTH: 29729 base pairs
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COMPUTER READABLE FORM:
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N: EXPRESSED IN HERRY, SIGNAL = 2.4
N: EXPRESSED IN BRAIN, SIGNAL = 2.4
N: EXPRESSED IN BRAIN, SIGNAL = 1.8
N: EXPRESSED IN PLACENTA, SIGNAL = 1.8
N: EXPRESSED IN HEA, SIGNAL = 3
N: EXPRESSED IN PETAL LIVER, SIGNAL = 2.9
N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
                     PRIOR APPLICATION NUMBER: PCT/USC1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USC1/C0661
PRIOR APPLICATION NUMBER: PCT/USC1/C0670
PRIOR APPLICATION NUMBER: PCT/USC1/C0670
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-29
NUMBER OF SEQ 1D NCS: 49117
SEC ID NO 82044
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ORGANISM: Homo sapiens
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US-09-613-486-15 (1-198) x US-09-759-508B-1 (1-81940) Ov 54 LeuTyrAlaLeuAlaArdTürThrSer	64723 GTATACACAGGAAGCCAAAAATGCATCTGCAAAAGCAGAAATTAAAGTGAAA 6478 66 ValglaargalaaspSeraspValile	Ob 64783 GTACAAGATACACCAGGAAAAGTAGTTGGGCCAATAAGATTCACCAATATTACTGGGGAG 64842 Qy 82 ArgAsnValValThrGluGlyAspteulysiysValLeuAspGlyCysAlaProLeu 161	102 ThrArgPheThrAssisysLewargThrPheGlyArgThrPheThrGluAlaTyrValAsp	Cy 122 PhecysileA:a	Cy 129 LysLeuProGlnLeuAsnAlaAlaAlaCluLeuGlyIleProAlaGluAspSerTyrLeu 148 ::: ::::: ::::: ::::	Cy 149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGinSerArgLysMet 168	169 PheAlaSerMetTyrAlaLeu	184 ThrProValSerAsnieuArgGlnLeuGlyArgArgGlu 196	CCITGAAAGAAGAA 6521	Sequence 724, Application US/0987319A Sequence 724, Application US/0987319A Sublication No. US20030134324A1 Sublication No. US20030134324A1 Subplication No. US20030134324A1 Subplication Volumer. William E. APPLICANT: Winder, William E. APPLICANT: William E. APPLICANT: Waga. Iwao CURRENT FILING DATE: 2001-06-05 EARLIER APPLICATION NUMBER: US/09/873,319A CURRENT FILING DATE: 2000-08-07 KUMBER OF SEQ ID NOS: 755 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 724 LENGTH: 81940 TYPE: DNA CRGANISM: Homo sapiens FEATURE: COTHER INFORMATION: Genbank Accession No. US20030134324A1 X90568	A.ighment Scores: Pred No.: Pred No.: Score: Score: Percent Similarity: Best Local Similarity: Ouery Match: 12 Gaps: A.ighment Score Bridels: A.ighment Score Agaps: A.ighment Score Anismatches:
13176	Db 13236 CAGGAATTAGTTGCGTTATACCAAGAGAATCCTGACGTGCCATTGGTGCGGGGACAGTT 13295 Oy 54 LeutyralaleualaalaargthrThrSerProLysvalGlrargalaaspSerAspval 73 Db 13296 TTGGATGCTACGACTGCTTAGCTATTGTAGCAGGGGCTGAATAT 13343	Oy 74 IlePheSerAsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLys 93 Db 13344 ATTGTGAGTCCAAGGTTCSATGAAGAAACCGCTAAAATTTGCAATTTATATGAGTTCCT 13403	94 ValleuaspGlyCysAlaProLeuThrArgPheThrAshLySLeuArgThrPhe	112GlyArgIhrPhefhrSluAlaTyrValAspPheCysileAla 13464 ATTATTAAACTATTTCCGGAAGTGTTTATGGACCGAGTGTTATTCAGCA	126 TYFD/8H:SLYSCHUPFOGINGENARALAALAALULEUGIY/1EPFCALAGIUASE 13:1	13575	Qy 150 AlaAspPheLeuGlyThrCysProLysLeuSerGiuLeuGlnGinSerArgLysMet 168 	Cy 169 PheAlaSerYetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188	Oy 189 LeuhrgGinLeuGiyArgArgGiuVal 197 ::	RESULT 14 US-09-759-508B-1 i Sequence 1, Application US/09759508B i Sequence 1, Application No. US2022018259A1 j GENERAL INFORMATION: APPLICANT: Fishman, Mark C. TITLE OF INVENTION: Mcthodis for Diagnosing and Treating Heart Disease FILE REFERENCE: 00786/381002 CURRENT PAPLICATION NUMBER: US/09/759,508B CURRENT FILING DATE: 2203-01-12 PRIOR PILING DATE: 2203-01-12 PRIOR APPLICATION NUMBER: US 60/175,787 PRIOR PILING DATE: 2203-01-12 PRIOR PILING DATE: 2203-01-12 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SEQ TING: NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS OTHER INFORMATION: US-09-759-508B-1 Balinnmant Scores.	Prediment SCOIES: 2.22e+03 Length: 61940 Score: 75.00 Matches: 39 Percent Similarity: 37.71% Conservative: 27 Best Local Similarity: 22.29% Mismatches: 67 Ouery Match: 7.57% Indels: 42 DB:

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55071 GITGCTCAAATACAATATACTGTTCCTGATGCCCCTGGCATTCCAGAAACCTAGCAACATA 65130
                                                                                             64894 ACCCACTACATCATTGAAAACGGGAAACCAGCAGACTTGCCTGGGCACTAATTGAGGAT 64953
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                                                                                                                                                64843 AAGAIGACTCIGIGGIGGGAGCCCCACTCAT-----GACGGIGGTGCCCCATA 64893
                                                                                                                                                                                                                                                       129 LysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSerTyrLeu 148
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                                                                                                                                                                                 102 ThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAsp 121
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                                                                           ----PheSerAsnSerPheGlyGlu 81
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79.5 8.0 320 2 79 8.0 308 2 77.5 8.0 308 2 77.7 8 28 392 2 77 7.8 397 2 77 7.8 397 2 76.5 7.7 58 38 2 76.5 7.7 583 2 76.7 7.8 838 2 76.7 7.8 838 2 76.7 7.8 838 2 76.7 7 88 2 77.6 7 8 8 2 78.7 8 8 2 79.6 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	A A B B A B B A B B A B B A B B A B B A B B A B B A B B A B B A B B B A B B B A B B B B A B	ws virus irus, SBYV evision 06- ull, R. ull, R. ary, August nce of cDNF	i NID:93232 i Boyko, Vary, June 1 ide sequenc i NID:93136 i NID:93136 i Score 29	31; Pred: NC 31, Misma DKKLLSAEVEK COCKLRKNFEE NVVVTEGDLKK : : : ELFLTHGELRS	AEDSYLAADFI AEDHYLAADFI	ws virus irus, SBYV evision 07-
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                                          Expectational protein 2 - sugar beet yellows virus
Cispectes: sugar beet yellows virus
Cispectes: sugar beet yellows virus, SBYV
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
Cibate: 06-Jan-1995 #section: Nucleotide sequence of cDNA encoding the coat protein of beet A;Reference number: S27898
A;Reference number: S27898
A;Reference number: S27899
A;Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 SMYALKTEGGVVNTPVSNLRQLGR 194
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Best Local Similarity 25.08
Matches 50; Conservative
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                                      RiAgranovsky, A.A.; Boyko, V.P.; Karasev, A.V.; Lunina, N.A.; Koonin, E.V.; Dolja, V.V. J. Gen. Virol. 72, 15-23, 1991
A.Title: Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA AREference number: $287.0; MUID:91116305; PMID:1990061
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C/Species: citrus tristeza closterovirus CTV
C/Species: citrus tristeza closterovirus CTV
C/Accession: D49804
R/RPappu, H.R.; Karasev, A.V.; Anderson, E.U.; Pappu, S.S.; Hilf, M.E.; Febres, V.J.; B.K.; Pappu, B.S.; Hilf, M.E.; Febres, V.J.; B.W.; Dawoon, W.O.; Lee, R.F.; Niblett, C.L.
A/Title: Nucleodide sequence and organization of eight 3' open reading frames of the A/Reference number: A49804; MUID:94160579; PMID:8116253
A/Accession: D49804; MUID:94160579; PMID:8116253
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A/Accession: PAPP>
A/Residues: 1-223 APP>
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A;Note: severe quick decline isolate 136
C;Superfamily: SBYV probable coat protein
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X53462; NID:958878; PIDN:CAA37554.1; PID:958883
C;Superfamily: SBYV probable coat protein
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Best Local Similarity
Matches 56; Conserva
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-204 <AGR>
C, Accession: S28715
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98

Length 216;

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A.Molecule type: DNA https://doc.org/193396/2002-1000-193399 A.A.Scasdues: 1-:0802 < v2002-1000-19302-1000-19302-1000-19302-193039 A.Cross-references: GB:M26699, NID:g173338; PIDN:AAA35284.1; PID:g173339 B.Yamawaki-Kataoka, Y., Tamacki, T.; Choe, H.R., Tanaka, H.; Kataoka, T. P. Proc. Natl. Acad. Sci. U.S.A. 86, S693-5697, 1989 A.Fitle: A.Cross-reference in yeast: a comparison of the genes from Schizosaccharcmyce A.Fitle: Acanquate cyclases in yeast: a comparison of the genes from Schizosaccharcmyce A.Feterence number: A33539; MJID:89345533; PMID:2668944
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A.Cross-references: GB-M24942; NID:g173378; PIDN:AAA35301.1; PID:g173379
A.Cross-references: GB-M24942; NID:g173378; PIDN:AAA35301.1; PID:g173379
A.Note: the authors translated the codon TGC for residue 626 as Ser, and GCC for residue 7.Note: the authors translated the codon TGC for Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, June 1998
A.Reference number: Z21881
A.Accession: T3980
A.Accession: T3980
A.Accession: T3980
A.Accession: T3980
A.Accession: DAA
A.Accession: T3980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S. Science 234, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
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A;Cross-references: EMBL:AL023859; PIDN:CAA19571.1; GSPDB:GN00067; SPDB:SPRC19C7.
A;Experimental source: strain 972h-; cosmid c19C7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 TIMDI -----GADVLRKFSEKKITANLDISKSNLEVIPVKIYPYAHELISLNVSHNLSLD 443
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                                                                                                                                                                                                                                adenylate cyclase (EC 4.6.i.1) - fission yeast (Schizosaccharomyces pombe) C, Species: Schizosaccharomyces pombe C, Date: 23-War-1990 #sequence revision 23-Mar-1990 #text_change 31-Mar-2000 C, Accession: A33989, A33539; T3980 T3980; A3: T3988, MUD: 90046723, PMID: 2682634
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C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change :8-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 LIQENTERILL ---- PHEQPCIIFERLISLFGCKVTS ----- DEEINEEDNYSVARLVF
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9.3%; Score 92; DB 2; Length 1692;
Best Local Similarity 24.7%; Pred. No. 5.9;
Matches 42; Conservative 26; Mismatches 68; Indels
     214
SSVDGKIV----SLFDLGR
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     200
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A,Status: preliminary
A,Molecule type: genomic RNA
A,Molecule type: genomic RNA
A,Residues: 1.240 e PAP>
A,Cross-references: GB:U16304; GB:U32547; GB:L23760; NID:g306738; PIDN:AAC59629.1; PID:g
A,Note: sequence extracted from NCBI backbone (NCBIN:144092, NCBIP:144099)
A;Note: severe quick deciline isolate 736
C;Superfamily: SBYV probable coat protein
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A. Gen. Virol. 72, 15-23, 1991
A. A. Title: Nucleoride sequence of the 3'-terminal half of beet yellows closterovirus RNA A, Reference number: S28710; MUID:91116305; PMID:1990061
                                       C.Species: citrus tristera closterovirus CTV
C.Date: 11-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
C.Date: 12-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
C.Date: 12-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
R.Pappu, H.R., Karasev, A.V.; Anderson, E.J.; Pappu, S.S.; Hilf, M.B.; Febres, V.C.; B.S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.
Virology 199, 35-46, 1994
A.Title: Nucleotide sequence and organization of eight 3' open reading frames of the change of the chan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKFTGEHLKYVXVIMDTFLLENYKTKTEDLLVHLIMIÇK--------RLYTI--- 104
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hypothetical protein 5 - sugar beet yellows virus

C;Species: sugar beet yellows virus, SBYV

C;Species: 07-May-1993 #sequence_revision 07-May-1993 #text_change 10-Dec-1999
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A,Residues: 1-216 <AGR>
A,Cross-references: EMBL:X53462; NID:g58878; PIDN:CAA37553.1; PID:g58882
C,Superfamily: SBYV probable coat protein
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10.0%; Score 99.5; DB 2; Length 216;
Best Local Similarity 25.0%; Pred. No. 0.083;
Matches 50; Conservative 27; Mismatches 94; Indels 2
     capsid protein homolog p27 - citrus tristeza closterovirus CTV
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probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-101 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 (Species: D2-101) (Species: B44722 (Species: B44722 (Species: B44722 (Species: Moffat, M.S.; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999 (Arcession: B4472 (Arcession: B4472) (Arcession: B4
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probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84722
C;Accession: A84722
F;Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Benitc, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
                                                                                                                77 NSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLPQL 133
                                                                                                                                                                                                                                ----AYPIHMINNI 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 PFISGYODFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFC 214
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234 LSGTGKTTLSADADRKLIGDDEHGWSDTGVFNIEG-GCYAKCIHLSEEK----EPQIFNA 288
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A;Residues: 1-360 <STO>
A;Cross-references: GB:AE002093; NID:g4582449; PIDN:AAD24833.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                     134 NAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKM--FASMYALK---TEGGVVN 183
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tes 49; Conservative
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Rikunst, F.; Ggaswara, N.; Noszer, T.; Albertin., A.M.; Allon, G.; Azevedo, V.; Berter Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Hurbors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallex, Cectter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Jauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lu, Lu, F.; Maueell, Y. M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Darro, V.; Pohl, T.M.; Porcetelle, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Scanson, T.; Winters, S.; Wipat, A.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Gonica, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, K.; Yasumoto, W.; Yata, K.; Yoshida, A; A; Huthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Rite: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: F69673
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A)Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: virH:
A;Genome: plasmid
C:Superfamily: Agrobacterium plasmid cytochrome P450 pinFl; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;366/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                                   A.Residues: 11419 <KUR>
A.Cross-references: GB:AE008690; PIDN:AAL46386.1; PID:g17744179; GSPDB:GN00183
A.Experimental source: strain CS8 (Dupont)
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TFAFR------MIDALRPEITKLTEHLWJDVPRVDC--FDFAEMYASKLPALTIA 164
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A:Molecule type: DNA
A:Residues: 1-527 <KUN>
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.1%; Score 90; DB 2; Length 419; 1 Similarity 25.1%; Pred. No. 1.5; 52; Conservative 26; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.8%; Score 87; DB 2; Length 527; Best Local Similarity 26.9%; Pred. No. 3.9; Matches 47; Conservative 24; Mismatches 70; Indels
A; Reference number: AB2577; MJID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: phosphoenolpyruvate carboxykinase (ATP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 -FASMY--ALKTEGGVVNTPVSNLRQL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AELGIPAED-----
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                                                                                                    A;Status: preliminary
A;Molecule type: DNA
                                                           A; Accession: AD3246
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A.Accession: G7521
A.Status: preliminary
A.Noiceule type: DNA
A.Noiceule type: DNA
A.Fesidues: 1-447 «KAW»
A.Cross-references: GB:AJ48283; GB:AJ096836; NID:G5457433; PIDN:CAB49062.1; PID:e15149
C.Senetics: Dp; PABC087
C.Senetics: Dp; PABC087
C.Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-729 <BLAT>
A,Cross-references: GB:AE000348; GB:U00096; NID:g1788975; PIDN:AAC75675.1; PID:g1768980
A,Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-729 cPUD.
A; Residues: 1-729 cPUD.
A; Residues: 1-729 cPUD.
A; Cross-references: EMBL: U36840; NID:g1033110; PID:g1033122
A; Cross-references: EMBL: U36840; NID:g1033110; PID:g1033122
A; Cross-references: EMBL: U36840; NID:g1033110; PID:g1033122
A; Esperimental source: strain kl2, substrain MG1655
B; Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Reset, D.T.; Mau, B.; Shac, Y.
A; Tit.e: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:g7426517; PMID:g278503
A; Rocession: E65041
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
      Rianonymous, Genoscope submitted to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 specification: Pyrococous abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 ARLPSTPETIYGIGSITKSFTALAIMKLVEEGGLS--LDD--PVEKFVNIKLRPFGEPVT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YVDFCIAYK--HKLPQLNAAAELGIPAEDSYLAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KLESFIVEKMAERK-VPGISISII-------KDGDVVYAKGFGYRNVE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Escherichia coli
C;Date: 1:-Jun-1999 #sequence_revision 1:-Jun-1999 #text_change 01-Mar-2002
C;Accession: T08639; E65041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VVTEGDLKKVLDGCAPLTRFTN-KLRTFGRTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 RITSPKVQRADSDVIFSN---SFGERNV--VVTEGDLKKVLDGCAPLIRFINKLRIFGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ELMSDSNLSNLVI--TDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 KLLSAEVEKKLVQKGAPNEGIEVVFGLLLYALAARTTSPKVGRADSDVIFSNSFGERNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; 3aps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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8.6%; Score 85.5; DB 2; Length 729;
Best Local Similarity 22.4%; Pred. No. 8.1;
Matches 41; Conservative 31; Mismatches 64; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 86; DB 2; Length 447;
26.0%; Pred. No. 3.9;
Live 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein b2627 - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 EAYVDFCIAYKHKLPÇLNAAAEL -- GIPAEDSYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VHHLLTHSSGIPSLGYAEAFIJGMVGGDNWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1995 A;Reference number: 216465 A;Reference number: A;Accession: 196839 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.0%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 FTEA-----
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                                                                                                                                                                                                                                                                       137 SEQPNMFKSYTARLKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRALEYPFISG 196
                                                                                                                                                                                                                                                                                                                                    61 TISPKVQRADSDVIFSNSFGERNVVYTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                              197 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLFI-HMTAKFRNIFRFCLEHHN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DECIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 GHSHPVFSGDRVHBFAMKLAGAIYMEVQQAGGGIMFTIN---KTREASEQDLRKDFEELA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLIRFINKLRIFGRIFTEAYVDFCIAYKHKLPQLN--AAAELGIPAEDSYLAADFLG--T 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KKMLRSGTTTLEAKSGYGLNVDAEMKMLRVLATENPNIPLE---VSATFCGAHA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1-445 <LLAT>
A.Cross-references: EMBL:U13019; PIDN:AAC24449.1; GSPDB:GN00021; CESP:T12A2.1
A:Experimental source: strain Bristol N2; clone T12A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MELMSDSNLSNLVITDAS-----SLNGVDKKLLSAEVEKMLVQKGAPNEGIEV---- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ----VF-GLLLYALA---ARTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 IKILNDSSNSLVILVDTNGKFSYIGNLNGAENKLKGEGVEMENLKIIDSSNGGIAIPGFVD
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A:Introns: 33/3; 117/3; 146/3; 202/3; 250/2; 297/3; 371/1; 407/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 445;
                                                                                             Jength 360;
                                                                                   Query Match 8.7%; Score 86; DB 2; Length 360
Best Local Similarity 26.5%; Pred. No. 2.9;
Matches 49; Conservative 23; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 VPKGSTEYEQTRXICEELIPKIEDEKRNGGLKN--VENI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.7%; Score 86; DB 2; Best Local Similarity 24.7%; Pred. No. 3.8; Matches 54; Conservative 41; Mismatches 80
                            C, Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: CESP:T12A2.1
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A; Map position: 2
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7.4 407 1 PEPT STRPY C9aCf4 7.4 657 1 TKT RHOSH P29277 7.4 707 1 ORC SCHPO P54789 7.4 862 1 SLAZ BACAN P944789	7.4 1051 : APSB_EMENI	249530 035874 029230 C9m2q4	7.3 278 1 PROC VIBAL PS2053 7.3 496 1 AMYB_TRIRP C65015	ALIGNYENTS		STANDAR	01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update)	<pre>Coat protein. Cirrus tristeza virus (isolate T36) (CTV). Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae; Closterovirus.</pre>	BI_Tax:D=31712;	SEQUENCE FROM N.A., AND SEQUENCE OF 27-38. MEDLINE=9123734, PubMed=203386; Sekiya M.E., Lawrence S.D., McCaffery M., Cline K.; "Molecular cloning and nucleotide sequencing of the coat protein gene	citrus tristeza virus."; Gen. Virol. 72:1013-1020(1991),	QUENCE FROM N.A.	DLINE=941605/9; FUDMEd=8116253; ppu H.R., Karasev A.V., Anderson E.J., Pappu S.S., Hilf M.E.,	Dies V., Eckloti K.M.G., Mccattery M., Boyko V., Gowda S., Jav. V., Koonin E.V., Manager and Manager a	ucrective sequence and organization of eight 5 open leading limits the citrus tristers closterovirus genome.";	ALL ALLOY 1973-39-19(1994). CC -!- PTM: CONSISTS OF ALL LEAST TWO SIZE VARIANTS, CP1 AND CP2, WHICH CC -RESULT OF POST-TRANSLATIONAL PROTEGLYSIS AT SITES APPROXIMATIVELY	12 TO 15 AND 26 AA FROM THE N-TERMINUS RESPECTIVELY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -	e European Bioinformatics Institute. There are no restrictions on its	diffied and this statement is not removed. Usage by and for commercial	calles requires a license agreement (see actp://www.isb-sib.cn/announce/send an email to license@isb-sib.ch).	BL; M76485; AAA4224.1;	<pre>EMBL; Ule304; AAC29630.1; InterPro; IPR002679; Closter_coat.</pre>	PF01/85; Closter_coat; 1. protein.	223 AA; 24909 MW; 00493F3D330220BB CRC64;	Ouery Match 12.6%; Score 125; DB 1; Length 223; Best Local Similarity 25.9%; Pred. No. 0.00025; Watchee 67. Corestruative 33. Manachee 63. Indele 62. Cone 10.	יי סייספו ישרניים ייודטוומרכיים סרי דוותפום סרי למקט ייס	SSLN-GUCKKLESA-EVERMLVOKGA	29 SSVNLHIDFILLIMNDVRQLSTQQNAALNRDLFLTIKGKHPNLFDKOKOFFIJAMNLYRLA 58 59 ARTTSPKVQRADSDVIF-SNSFGERNVVVTEGDLKKVLDGC 98	
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen	earch, using sw model	er 7, 2003, 14:45:43; Sear (withou 547:723	613-486-25 SDSNLSNLVITDASSL	162 10.0 , Gapext 0.5	seds,	atisfying chosen parameters:	200000000	um March O% um March 100% ng first 45 summaries	Prot_41:*	number of results predicted by an or equal to the score of the y analysis of the total score di	SUMMARIES	արագրի ըթ	0.00 L 000				н н				٠,٠		4 ~ ~	- н -		536 I PPCK BRUME 536 I PPCK BRUSU 863 I CLPB SYNP7		t	1 SPSY 1 YY00	
Copy	OM protein - protein se	Run on: Novembe	Title: US-09-(Perfect score: 991 Sequence: 1 MELM	Scoring table: BLCSUM6 Gapop 1	Searched: 127863	Total number of hits sa	Minimum DB seq length: Maximum DB seq length:	Post-processing: Minimum Maximum Listing	Database : SwissProt	Pred. No. is the number score greater than or er and is derived by analy:	d	ery	105 10 6	92 9.	87 87 80	83.5 8.	83 83 8.	0 81.5 8.	3 79 8.	79 8.	7.0	78.5 7.	76.5 7.	76 77.	75.5 7.	25 75 7.6 26 75 7.6 27 75 7.6	9 74.5 7.	74.5 7.	3 73.5 7.	

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CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate. COFACTOR: Binds 1 magnesium ion per subunit (By similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLATE CYCLASES 2; 1.
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LRR 5.

LRR 5.

LRR 9.

LRR 9.

LRR 10.

LRR 11.

LRR 12.

LRR 12.

LRR 14.

LRR 16.

LRR 17.

LRR 18.

LRR 19.

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InterPro; IPR001932; PP2C-like.
InterPro; IPR001932; PP2C-like.
InterPro; IPR001159; RA_domain.
Pfam; PF004011; guanylate_cyc; 1.
Pfam; PF00481; PP2C; 1.
SWART; SX00349; LRR TYP; 1.
SWART; SX00349; LRR TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                GeneDB SPombe, SPBC19C7.03, -. InterPro, IPR001054, G_cyclase.InterPro, IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                              EMBL; AL023859; CAA19571.1; -. PIR; A33988; A33988.
                                                                                                                                                                                                                                                                                                             EMBL; M26699; AAA35284.1; -.
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Conservative 2
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PROSITE; PS50200; RA;
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es 42; Conserv
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                                                                          MEDLINE=89345533; PucMed=2668944; Yamawaki-Kataoka Y., Tamacki T., Choe H.-R., Tamaka H., Kataoka T., "Adenylate cryclasess in yeast: a comparison of the genes from Schizosaccharomyces pombe and Saccharomyces cerevisiae."; Proc. Natl. Acad. Sci. U.S.A. 86:5693-5697(1989).
                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Plays essential roles in regulation of cellular metabolism by catalyzing the synthesis of a second messenger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90046723; PubMed=2682634;
MEDLINE=90046723; Pield J., Vojtek A., Broek D., Wigler M.;
"The adenylyl cyclase gere from Schizosaccharomyces pombe.";
Proc. Nati. Acad. Sci. U.S.A. 86:7989-7993(1989).
                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                           159 LSELQQSRKMFASMYALKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                             185 LIDLECAVYIQAKEQLIK-KRGADIVVVINVRÖLGK 219
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                              CYRI OR SPBC19C7.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation—the between by a bioinformatics Institute. There are estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNVVV 86
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-:- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-:- ENZYME REGULATION: In contrast to yeast cyclase, S.pombe cyclase is not likely to be regulated by RAS proteins.
-:- SIMILARITY: Belongs to the adenylyl cyclase class-3 family.
-:- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
-:- SIMILARITY: Contains 1 PP2C-like domain.
-:- SIMILARITY: Contains 1 Ras-associating domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.3%; Score 92; DB 1; Length 1692; 24.7%; Pred. No. 3.1; ve 26; Mismatches 68; Indels
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80 MAGNESIUM (BY SIMILARITY).
190333 MW; D137CBE8770A8655 CRC64;
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Bacteria;
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                              TIMDI - - - - GABULRKFSEKKITANLDISRSNLEVIPVKIYPYAHELISLNVSHNLSLD 443
TEGDLKKVIDGCAPLTRFTNKLRT----FGRTFTBAYVDFCIAYKHKLPQINAAAELGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE (POTENTIAL).
ACID EXTRACELLUIAR PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                     Yarrowia lipolytica (Candida lipolytica).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97039861; PubMed=8885407;
Young T.W., Wadeson A., Glover D.J., Quincey R.V., Butlin M.J.,
                                                                                          ----LPLDFMERCVKLKRLDISNN-----LRSPRG---KPITALRCL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                             "The extracellular acid protease gene of Yarrowia lipolytica: sequence and pH-regulated transcription.";
Microbiology 142:2911(1996).
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 89.5; DB 1; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF3002b; asp, ...
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 1.
Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
Hydrolase; Aspartyl protease; POTENTIAL.
                                                             143 AEDSYLAADFIGTCPKISELQQSRKMFASMYALKTEGGVVNTPVSNLRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DINKED (GLCNAC. . .) (PC BD678814B4B8984F CRC64;
                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acid extracellular protease precursor (EC 3.4.23.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.91;
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397 AA;
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les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4952;
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Q92389;
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Matches
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72 DVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTE-AYVDFCIAYKHKL 130

TDNAVIGGA-----SAPGFKFGVNSGDLSSGGFSMVFGIGVNSDASTSISAQLQKSGEIS TDASSLNGVDKKLLSAEVERMLVQKG-APNEGIEVVFGLLLYALAARTTSPKVQRAD--S

41;

86; Indels

Conservative

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A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Baroiser L., Brans A., Braun M., Brignell S.C., Bron. S., Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Arouilet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A., R. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entizot. D., Ernington J., Fabret C., Francis E., Foulger D., Am., Fulta M., Fulta M., Fulta M., Fulta M., Galleron N., Achibert H., Holsapel S., Hosono S., Haicch J., Harwood C.R., Henaut A., Anibert H., Holsapel S., Hosono S., Klaerr-Blanchard M., Xlein C., Acosyashi Y., Koerter P., Kohingstein G., Krogh S., Kumano M., Acosyashi Y., Koerter P., Maruno M., Medigue C., Acosyashi Y., Koerter P., Mizuno M., Mosell D., Nasala S., Kumano M., Acosyashi Y., Koerter P., Mizuno M., Mosell D., Nasala S., Mauel C., Medigue C., Acosyashi Y., Koelly M., Ogawa K., Cgiwara A., Oudega B., Park S.H., Arescan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rescan E., Pulic P., Purnelle B., Rapoport G., Rey M., Sachor B., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Takagi T., Takahara H., Takemaru K., Ashura M., Tamakoshi A., Tanaka T., Tarkamar H., Weitzeneger T., Awandochi M., Tamakoshi A., Tanaka T., Tarkamar F., Vasamoto K., Yasumoto K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacilus F., Whiters P., Willer B., Schleich S., Schroeter R., Brochila K., Poshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacilus
-----TCPKLSELQ
                                                                                                   251 GDVDLFDNDLVILDSGTTYTYLKSDYYNAFLGGLEDLDITLSDYSGGWHGYPCSENSKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98048467; PubMed=9387221;
Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region.";
Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                             PPCK_BACSU STANDARD; PRT; 527 AA.
524134, 034304;
61-6CT-1596 (Rel. 34, Created)
15-JUL-1938 (Rel. 36, Last sequence update)
15-JUL-1938 (Rel. 41, Last annotation update)
Phosphoenolypruvate carboxykinase (APP) (BC 4.1.1.49) (PEP earboxykinase (Phosphoenolpyruvate carboxylase) (PEPPCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Firmicutes, Bacillales, Bacillaceae, Bacillus.
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MEDLINE=96345628; PubMed=8755891;
Yocum R., Perkins J.B., Howitt C.L., Pero J.;
                                                                                                                                                                 164 ----- OSRKMFASMYALKTEGGVVNTPVSN 188
                                                                                                                                                                                                           311 FTYNFSGKEITVTGHDLAIPGNAVNSNVDS 340
                                                                  131 PQL----NAAAELGIPAEDSYLAAD----FLG-
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151 DFL 153
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    complete
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Best Local S
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Q9ZNH4;
                             Science
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EXBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 IRFGSVLENVVVDED-----TREANYDDSFYTENTRA-----AYPIHMINNI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFGIAYK-HKLPQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P2259; layL.
Subtilist; BG1841; pckA.
HAMAP; MF 00453; -1.
InterPro; IPR001272; PEPCK ATP.
Ffam; PF01299; PEPCK ATP.
From; PF01299; PEPCK ATP.
TIGRFAMS; TIGR00224; pckA:
TIGRFAMS; TIGR0023; PEPCK ATP; 1.
Gluconeogenesis; byase; Decarboxy,ase; ATP-binding; Complete proteome.
NP_BIND.
233 240 ATP (BY SIMILARITY).
                        adenosylmethionine synthetase from Bacillus subtilis.";
J. Bacteriol. 178:4604-4610(1996).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNGVDKKLLSAEVEKMLV---OKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 NAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKM--FASMYALK---TEGGVVN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 VTPSMAGHPSAIVFLTADAFGVLPPISKLTKEQVMYHFLSGYTSKLAGTERGVTS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=KI2 / MG1655,
MEDLINE=97426617; PubMed=9278563;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 87; DB 1; Length 527; 26.9%; Pred. No. 2.2;
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Clouing and characterization of the metE gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).
L -> S (IN REF. 3).
ESSIEEC802D1E666 CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yfjk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF008220; AAC00377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 AA; 58300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z99119; CAB15034.1; -. EMBL; U52812; AAB17065.1; -.
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Best Local Similarity 26.99
Matches 47; Conservative
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ID YFJK_ECOLI
AC P52126;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 FTEA-------YVDFCIAYK--HKLPQLNAAAELGIPAEDSYLAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 LPKVLSLMEDVVKHHAVKRGIRSKVDYTHVKLAFESFHLPPGVNALEEIGIPIQTLHRLV 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       palustris no. 7 phosphoenolpyruvate carboxykinase gene.";
J. Bacteriol. 181:2689-2696(1999).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- PATHWAY: Rate-limiting gluconeogenic enzyme.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING LOG PHASE WITH 10-20 FOLD REDUCTION AT ONSET OF STATIONARY PHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inui M., Nakata K., Roh J.H., Zahn K., Yukawa H.;
"Molecular and functional characterization of the Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brādyrhizobiaceae; Rhodopseudomonas.
genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001650, .....
Pfer; Pr00271; helicase C; 1.
SNART; SW00480; DEXDC; 1.
SNART; SW00490; HELICC; 1.
Hypothetical protein; Complete proteome.
Arybothetical protein; Complete pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.6%; Score 85.5; DB 1;
(2.4%; Pred. No. 4.4;
ve 31; Mismatches 64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-EBB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003348; AAC75675.1; -. PIR; TC8639; TC8639. Ecodean; EC13197; Yf2. Ecodean; IPR001410; DEAD. InterPro; IPR001650; Helicase_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U36840; AAA79796.1; -.
                                                                  277:1453-1474 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 -STRFGAVLENVVLGDIJRKPDFJDGSK----TENTRS-----AYPLESIP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 NASLIGRAGOPKNVMLAADAFGVMPPIAKLIPAQAMYHFLSGYTAKVAGTERGVTEFIP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 LSGTGKTTLSADPNRTLIGDDEHGWGKDGVFNFEGGCYAKCIKLSAENEPEIYAA---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLL--LYALAARTTS---PKVQRADSDVI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 FSNSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 OLNAAABIGIPAEDSYLAADFIGTOPKLSELOOSRKY--FASMYALK---TEGGVVN-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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BDDLINE=20445131; PubXed=10993377;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P22259; IAU2.
R HAMAP; MF_00453; -; 1.
R InterPro; IPR001272; PEPCK ATP.
R Prodom; PD004723; PEPCK ATP.
DR TIGRPAMS; TIGR00224; pcKa.1.
DR PROSITE; P805523; PEPCK ATP; T.
DR PROSITE; P805523; PEPCK ATP; T.
DR PROSITE; P805523; PEPCK ATP; T.
DR PROSITE; P805523; PAPCK ATP; FALSE NEG.
KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding.
TIGRPAMS; TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; pcKa.1.
TIGR0024; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 84; DB 1; Length 537; 26.7%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NACUTE 407:81-86(2000).
-!- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
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InterPro; IPR002510; PmbA_TldD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB015618; BAA34956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera sp. APS.";
Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TldD protein homolog. TLDD OR BU398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=118099
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P57478;
g
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                                                                                                                                                                                                                                                                                                    104 FINKLRIFGRIFTEAYVDFCIAYKHKLPQLNAAABLGIPAEDSYLAADFLGTCPKLSELQ :63
                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 MTN-----YAVNFSG---GOVDIT 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEN S.-X.; Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Yiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia, J., Tu Y.-F.,
Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Man M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Sometville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ģ
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-:- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-:- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e.,
capable of catalyzing only the fifth step of the arginine
                                                                                                                                                                                                                                                           -GCAPLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotations update)
15-SEP-2003 (Rel. 42, Last annotations
16-SEP-2003 (Rel. 42, Last annotations
1
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               simlarity).
--- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-
ornithine + N-acetyl-L-glutamate.
--- CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Catalyzes two activities which are involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate.
-:- PATEWAY: Argimine biosynthesis; first step.
-:- PATHWAY: Argimine biosynthesis; fifth step.
-:- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
                                                                                                                                                                                                 45;
                                                                                                                                 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unique physiological and pathogenic features of Leptospira
                                                                                                                                                                                                 Indeis
                                                                                                                                 Length
                                                                52977 MW; A05CE98518720EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 CSRKMFASKYALKTEGGVVNTPVSNLRQLGR-REVM 198
                                                                                                                      1.arity 20.5%; Score 83.5; DB 1; 20.5%; Pred. No. 4.1; Conservative 26; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 SGKFVFSTSEAYLIKNGKIVTPIKNTTLIGSGLEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the arg. family.
                                                                                                                                                                                                                                                              65 KVORADSDVIFSNSFGERNVVVTEGDLKKVLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
Pfam; PF01523; PmbA_TldD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                 Complete proteome.
SEQUENCE 483 AA;
                                                                                                                             Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARGC LEPIN
QSEYVS;
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SO KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 LQIYPG----TLPVKEANPETLKKLSEYLKNYTEISLNVVLNVGTISMKFWGC----- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 TKLIELTISGAKSEAQARKIGKSILNSPLVKTAIYGGDPNWGRLIMAVGKVFDEPIPFEG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEVVFGLLLYALAARTTSPKVQAADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN ARGJ ALPHA CHAIN (BY SIMILARITY).
ASAININE BLOSVYTEBEIS BITUNCTIONAL
PROTEIN ARGJ BETA CHAIN (BY SIMILARITY).
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Raul R., Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Raul R., Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Raul R., Monks D.E., Almeida M.F. Jr., Woo L., Chen Y., Zhou Y., Chen L., Mood G.E., Almeida M.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Kutyavin T., Clendenning J., Dearherage G., Gillet M., Grant C., Rutyavin T., Levy R., Mandinachak C., Ru Z., Romero P., Gordon D., Raymond C., Rouse G., Saenphimmachak C., Ru Z., Romero P., Gordon S., Yoo H., Tao Y., Biddle P., Jung M., Krespan M., Perry X., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               ARGININE BIOSYNTHESIS BIFUNCTIONAL
                                                                                                                                                                      EMBL; AE011564; AAN51303.1; -.
HAMRP; MF 01106; -; 1.
InterPro; IPROC2813; ArgJ.
Pfam; PF01960; ArgJ; 1.
ProDom; PD034193; ArgJ; 1.
ProDom; TGRO0120; ArgJ; 1.
ArgJinne biosynthesis; Miltifunctional enzyme; Transferase; Acyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
PCKA OR ATU0035 OR AGR_C 56.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteologiceria; Alphaproteologiceria; Rhizobianes;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.1.1.49) (PEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 83; DB 1; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8A525296D0AD7C2F CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase (ATP) (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 21.3%; Pred. No. 3.4; Matches 29; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AA; 41445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 NKLRTFGRTFTEAYVD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385
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O8UJ94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PCK_AGRT5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 LSGTGKTTLSADPARTLIGDDEHGWGEHGIFNFEGGCYAKAIKLSSEAEPEIYAA---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 FSNSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AYPLHFIP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00453; -: 1.

InterPro, IPR01272; PRPCK ATP.

Pfam, FF1293; PEPCK ATP.

IIGRPAMS; TIGR00224; PEFCK ATP; 1.

PROSITE; PS00532; PEPCK ATP; 1.
                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase (ATP) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 INGVDKKILSAEVEKMLVQKGAPNEGIEVVFGLL--LYALAARTTS---PKVQRADSDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 QLNAAAELGIPAEDSYLAADFLGTCPKLSEL--QOSRKMFASMYALK---TEGGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAINEME / JCM 11007;
MEDLINE-21992816; PubMed-11997336;
MEDLINE-21992816; PubMed-11997336;
Bao Q. Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xu Y., Xu Y., Lai X., Huang J., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flandsan C., Crowell C., Gutson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome Sequence of the plant pathogen and biotechnology agent Agrobacterium tumefeaciers C58";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Clostridia; Thermcanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%; Pred. No. 5.1; ative 18; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 -TNRFGTVLENVVLDESRVPDFNDN--SLTENTRS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acctate kinase (EC 2.7.2.1) (Acctokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003946; AAK85859.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity 26.99
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=119072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACKA_THE
Q8R9V4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO THE TRANSPORT OF THE
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IPR001984; Lon_endopep.
IPR004815; Lon_fam.
                                                                                                                                                                                                                 EMBL; AEGG1162; AAC66962.1; -. PIR; D70176; D70176.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PFC0004; AAA; 1.
Pfam; PF02190; LON; 1.
Pfam; PF05362; Lon C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                 MERCPS; S16.UPW; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     TIGR; BBC613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSY_MOUSE
ID_SPSY_MOUSE
AC_P97355;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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Best Local S
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- KLRIFGRIFIE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 GGEYFIDSVIIDDEVIKK-LEDČIDLAPLHNPANIEGIKACQQIMPGVPMVAVFDTAFHQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KHKLPQINAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 TWPDYAYIYPIPYEYYEKHRIRRYGPHGTSHKYVSMRAABILGRPIEELKIVTCHLGNGA 213
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STRAINS—ATCC 35210 / B31;
STRAINS—ATCC 35210 / B31;
STRAINS—ATCC 35210 / B31;
MEDLINS—98065943; Pubmed-9403685;
Fraser C.W., Casjens S., Huang W.M., Sutten G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougharty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N.D., Gocayne J.D., Weidman J.,
Utterback T., Waithey L., McDonald J., Artiach P., Sowman C.,
Garland S., Fulii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GVDKKLLSAEV---FKMLVQKGAFN--EGIEVVFGLLL-YALAARTTSPKVQRADSDVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
                      -!- PATHWAY: Conversion of acetate to acetyl-CoA; first step. -!- SUBCELLULAR LOCATION: Cytoplasmic (8y similarity). -!- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01075; ACETATE_KINASE_1; 1.
PROSITE; PS01076; ACETATE_KINASE_2; 1.
TAGNSTE1285; Kinase; Complete protecome.
SEQUENCE 401 AA; 44361 WW; FD710642F1E019B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SNSFGERNVVYTEGDLKKVLDGC---APLTRFTN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP-dependent protease ia homolog (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:580-586(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%; Score 81.5;
19.3%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 KLSELQQSRKMFASMYALKTEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00871; Acetate kinase; 1.
TIGRFAMs; TIGR00016; ackA; 1.
                                                                                                                                                                                                                                                                                                                                  HAMAP; MF C0020; -; 1.
InterPro; IPR00089C; Acetate kin.
InterPro; IPR004372; Acka.
                                                                                                                                                                                                                                                                                                           EMBL; AE013105; AAM24700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 AYVDFCIAY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 40; Conserv
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051558;
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N2_BORBU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 NESN-LVITDASSINGVDKKLLSAEVEKMEVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 Q-RADSDVIFSNSFGERNVVVTEG--DLKKVLDGCAPLTRFTNKLRTFGRTFTEAY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 YIRIEDDVIFNLI---RNYTMESGVRGLKRVL------TNLIRRLVRELLYEY 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Spermine synthase (EC 5.1.22) (Spermidine aminopropyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                               Final, PP0219U; L. S. Billion C; 1.

R PAINTS, PR00362; Lon C; 1.

R PAINTS, PR00382; AAA; 1.

DR SMART; SM00464; LON; 1.

DR TIGRFAMS; TIGR00763; lon; 1.

DR TIGRFAMS; TIGR00763; lon; 1.

DR TIGRFAMS; TIGR00764; LON_SER; 1.

WHY Arcolase; Serine procease; ATP-binding; Complete proteome. ATP (POTENTIAL)

ND BIND 369 376 ATP (POTENTIAL)

ND BIND 719 MW; 5129AA1498G5DDF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,
Lehrach H., Mettinger T.;
"Pex agene deletions in Gy and Hyp mice provide mouse models for
X-linked hypophosphatemia.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Diaphragm;
Nizzanen K., Korhonen V., Janne J.;
"Nucleotide sequence of mouse spermidine aminopropyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.2%; Score 81.5; I
idarity 31.9%; Pred. No. 12;
Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                   InterPro, IPR003593, AAA ATPase.
InterPro, IPR003959, AAA ATPase_centr.
InterPro, IPR003111; LON.
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HSSP, P04391, 1AKM.
InterPro, IPR006130, Asp/Orn_COtranf.
InterPro, IPR02292; Orn_carbtransf.
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InterPro; IPR006132; OTCace P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D64006; BAA10847.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace N;
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Best Local Similarity
                                                                                                                                                                                                                                                                               L-citrulline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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P24466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 DGRLVEYDIDEVVYDEDSPYONIKILHSKQFGNIL-----ILSGDVNLAESDLAYTRAI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                             MEDLINE=98133937; PubMed=9467015;
LOVEDT B., Francis F., Gempel K., Boeddrich A., Josten M., Schmahl W.,
Schmidt J., Lehrach H., Melinger T., Strom T.M.;
"Spermine deficiency in Gy mice caused by deletion of the spermine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 MGSGKEDYTGKDVLILGGGDGGILCEIVKLKPKAVTMVEIDQMVIDGCKKYMR-----RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 CGDVLDNLRGDCYQVLIEDCIPVLKMYAKEGRBFDXVINDLTAVPISTSPEEDS--TWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 DKKLLSAEVEKMLVQKGAPNEGIEVV----FGLLLYALAARTTSPKVQRADSDVIFSNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------KVLDGCAPLTRFTNKLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                 synthase gene.";
Hum. Mol. Genet. 7:541-547(1998).
-!- CATALYTIC ACTIVITY: Spermidine = 5'-
=:- CATALYTIC ACTIVITY: Spermine + spermidine = 5'-
=:- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERVIDINE.
-!- PATHWAY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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15-JJL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyitransferase, anabolic (EC 2.1.3.3) (OTCase)
ARGF OR SLL0902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRIILDLSMKVLKÇDGKYF-----TQGNCVNLTEALSLYEEQLGR 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AA; 41313 MW; DS49F319F51C43C5 CRC64;
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NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 6.1; 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:109490; Sms.
GO; GO:0008215, P:spermine metabolism; IM
Interpro; IPR001045; Sprmine synthase.
Pfam; PF01564; Spermine synth; 1.
PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 80; 22.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Y09419; CAA70573.1; -. EMBL, A70010093; CAA031911; -. EMBL, AJ0000087; CAA03181; -. EMBL, AJ0000089; CAA03918.1; -. EMBL, AJ0000089; CAA03918.1; -. EMBL, AJ0000099; CAA03918.1; JOINED. EMBL, AJ0000091; CAA03918.1; JOINED. EMBL, AZ000092; CAA03918.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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SEQUENCE OF 316-366 FRCM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 22.98 52; Conservative
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OTCA_SYNY3
Q55497;
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SEQUENCE Query Match Best Local Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 LSAEVEKMLVQKGAP-NEGI-----EVVFGLLLYALAARTTSPKVQRADSJVIFSNSFGE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 RNVVVTE-GDLKKVLDGCAPLTRFTNKL--RTFGRTFTEAYVDFCIAYKHKLPQLNAAAE
MEDLINE=96127529; PubMed=8590279; Kareko T., Miyajima N., Kareko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Saguina M., Tabata S., Stoomers Synchroza analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTIEBMKSLLQLAADLKSGVLKPHCRKILGLLFYKASTRT---RVSFTAAMYQLGGQVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 79; DB 1; Length 308; 24.8%; Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89213933; PubMed-2708311;
Kanemoto R.H., Powell A.T., Akiyoshi D.E., Regier D.A.,
Kerstetter R.A., Nester E.W., Hawes M.C., Gordon M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOTLIRANSFERASE; 1.
Arginine biosynthesis; Transferaes; Complete proteome.
SEQUENCE 308 AA; 33616 MW; C6CD2E4998592CFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Arginine biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-YAR-1992 (Rel. 21, Created)
01-YAR-1992 (Rel. 21, Last sequence update)
01-YAR-1992 (Rel. 21, Last sequence update)
Cytochrome P450-pinFl, plant-inducible (EC 1.14.-.-).
CYP103 OR PINFL OR VIRHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 LGIPAEDSYLAADFLGTCPKLSELQQSRKMFASWYAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CQILADLOTIKECFGKLEGL 152
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Search completed: l
Job time : 18 secs
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send ar email to license@isbs:ib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 --SFGERNVVVTSGDLKKVLDGCAP-LTRFT-----NKLRTFGRTFTEAYVDFCIAYK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 INGVDKKILSAEVEKMIVQKGAPNEGIE--VVFGLIJYALAARTISPKVQRADSDVIFSN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; MISJ36, J. 2006.

PRIR; ASJ306, ASJ306.

InterPro. 1PR001128; Cytochrome_P450.

PRIMTS; PR00385; P450.

PROSITE; PS00385; P450.

PROSITE; PS00386; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Electron transport; Heme; Plasmid.

Oxidoreductase; Monooxygenase; Electron transport; Heme; Plasmid.

METAL 369 189 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ". Bacteriol. 1712506-2512(1989).
-!- FUNCTION: NOT ESSENTIAL FOR VIRULENCE, BUT MAY BE INVOLVED IN THE DETOXIFICATION OF PLANT PROTECTIVE AGENTS AT THE SITE OF WOUNDED -!- INDUCTION: TRANSCRIPTIONALLY ACTIVATED IN THE PRESENCE OF WOUNDED PLANT TISSUE AND BY PLANT PHENCLIC COMPOUNDS, SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 GETHGKRRSGLSKAFSFRMVEALRPEIAKITECLWJDLGKVDDF--NFTEMYAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 HKLPQINAAABIGIPAED------SYLAADFIGTCPKLSELQ-----
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analysis of the plant-inducible locus pinf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels
                                                                                                                                                                                          -!- SIMILARITY: Belongs to the cytochrome P450 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 -- CSRKM--- FASMYALKT-- EGGVVNTPVSNLRQ1 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 ADSGRAMRDDFLSRY-LKAVREAGTL-SPIEEIMQL 252
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3.6%; Pred. No.
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MEDLINE=21886394; PubMed=11889109;
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Best Local Similarity 23.6%
Matches 51; Conservative
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SEQUENCE FROM N.A.
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NCBl_TaxID=76856;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as ing as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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HAMAR, MESSACIA, 1.

TICHEPERO, TRR001272; PEPCK ATP.

PEAM; PF01293; PEPCK ATP, 1.

PROSITE; PS00532; PEPCK ATP, 1.

PROSITE; PS00532; PEPCK ATP; 1.

PROSITE; PS00532; PPCK ATP; 1.

PROSITE ATP; PS00532; PPCK ATP; 1.

PROSITE ATP; PS00532; PPCK ATP; 1.

PROSITE ATP; PS00532; PPCK ATP; PPCK ATP; PPCK ATP; PPCK ATP; P
J. Bacteriol. 184:2005-2018(2002).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                             -:- PATTWAY: Rate-limiting gluconeogenic enzyme.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
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26.6%; Pred. No.
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Best Local Similarity
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C9e7m2 citrus tris C9e7m4 citrus tris C9pxc0 citrus tris Q9dqqqq citrus tris Q9dwxl citrus tris C9dwxl citrus tris C9dwxl citrus tris	citrus tri citrus tri citrus tri	citrus tri citrus tri citrus tri citrus tri	citrus tri citrus tri citrus tri citrus tri	citrus tri citrus tri	citrus tri citrus tri	citrus tri citrus tri citrus tri	citrus tri citrus tri citrus tri	in anino				stage; Closteroviridae;	.R., Gonsalves D.; srapevine Leafroll-	rus, the		CRC64;	<pre>Length 198; Indels C; Gaps 0;</pre>	SIEVVFGLLLYALAAR	SAPNEGIEVVEGLEYALAAR 60 PITRFTNKLRTFGRTFTEAYV 120		BELQOSRKMFASMYALKTEGG 180
17 123.5 12.5 223 12 09E7M2 18 123.5 12.5 223 12 09E7M4 19 123.5 12.5 223 12 09EXT0 20 123.5 12.5 223 12 09EXT0 21 123 12.4 212 12 09DWW1 22 123 12.4 212 12 09EWM3 22 125 12.4 212 12 09EWM3	120.5 12.2 222 12 120.5 12.2 223 12 120.5 12.2 223 12	120.5 12.2 223 12 120.5 12.2 223 12 120.5 12.2 223 12 120.5 12.2 223 12	120.5	115.5 11.7 223 12	115.5 11.7 223 12	114.5 11.6 223 12 114.5 11.6 223 12	113.5 12.5 194 111.5 12.3 223 110.5 11.2 223	10.00 0.11	ODD THANK TOO	10 0/1213 PRELIMANY; PKI; 198 AA. AC 071213;) DT 01-AUG-1998 (TrEMBLrel. 07, Created) DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat	DE 22 KDa coat protein. SS Grapevine leafroll-associated virus 2. OC Viruses; ssRNA positive-strand viruses, no DNA st OC Closterovirus. OX NCBI TaxID=64003;	RY SEQUENCE FROM N.A. RX MEDLINE=98.545.07; PubMed=9603345; RA Zhu H.Y., Ling K.S., Goszczynski D.E., McFerson J.R., Gonsalves D RT "Mucleotide Sequence and Genome Organization of Grapevine Leafrol	Associated Virus-2 are Similar t Closterovirus Type Member.";	The state of the s	Fidm; Frui/85; Closter_Coat; 1. Coat protein. SEQUENCE 199 AA; 21660 XM; REDBSEF2EF1DFB03	Query Match 100.0%; Score 991; DB 12; Best Local Similarity 100.0%; Pred. No. 7.7e-89; Matches 198; Conservative 0; Mismatches 0;		DD 1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKG CV 61 TTSPKVQRADSJVIFSNSFGERNVVVTEGDLKKVLDGCAF		Cy 12: DFCIAYKHKLPQUNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG
.1.6 ompuger Ltd.	rch time 34 Seconds ut alignments) 77 Million cell updates/sec	.GGVVKTPVSNLRQLGRREVM 198			:: 83C52 5								cted by chance to have a of the result being printed, score distribution.		ipta	071213 grapevine 1 039837 grapevine 1	099629 sugar beet 09664 sugar beet 08991C sugar beet	003312 sugar beer Q08531 sugar beet Q65358 beet yellow	08)yvl dittus tris Q9Geg4 dittus tris Q990p0 dittus tris	Q990p2 citrus tris Q9qeg5 citrus tris	Vebata citrus tris Q9qeg2 citrus tris
GenCore version 5.1 Copyright (c) 1993 - 2003 Comp protein search, using sw model	November 7, 2003, 14:46:13 ; Search (without a 1502.777 M	US-09-613-486-15 991 1 MELMSDSNLSNLVITDASSL	BLCSJM62 Gapop 10.0 , Gapext C.5	25 segs, 258052604 residues		length: 0 length: 2000000000	. Minimum Match 0% Maximum Match 100% Listing first 45 summaries	SPTREMBL 23:* 1: Sp_archea:* 2: Sp_bacteria:*	4: Sp. human: • 5: Sp. invertebrate: • 6: Sp. ammal: • 7: cp. http://www.near.ear.ear.ear.ear.ear.ear.ear.ear.ear.	/: sp_mc:* 8: sp_organelle:*	9: sp_phage:* 10: sp_plant:* 11: sp_rodent:*	12: Sp virus: 13: Sp vortebrate: 14: Sp unclassified: 15: Sp rvirus: 16: Sp bacteriap:	the number of results predict than or equal to the score dby analysis of the total	SUMMARIES	o Very Match Length DB ID	.0 198 12 3 198 12 9 108 12	30.0 204 12 090629 29.9 204 12 090664 29.8 204 12 0906664	.9 204 12 .9 215 12	.2 223 12 .1 223 12 .7 222 12	.7 223 12 .7 223 12 .6 223 12	6 223 12
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61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae; Closterovirus.
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Viruses; ssNAA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
VCBI_TaxID=167634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 198;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, Y4131; CAN74566.1;
InterPro; IPR002679; Closter.
Pfam; PF01785; Closter.coat.
SEQUENCE 198 AA; 21630 MW; 15D631E4088D3F01 CRC64;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 198 AA; 21620 MK; 370E95A9369734A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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99.3%; Score 984; DB 12;
Best Local Similarity 99.5%; Pred. No. 3.7e-88;
Matches 197; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           198 AA
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01-MAR.2003 (TrEMBLrel. 23, Last seq
01-NAR.2003 (TrEMBLrel. 23, Last anno
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                                                                                                         181 VVNTPVSNLRQLGRREVM
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Zhang Y., Rowhani A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=64003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8BEP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 SVQPTSTFIKASFGSGKELFLTHGELRSFLDSQKLLEGKPNKLRCFCRTFQKCYISFAKE 130
                                                                                                                                                                                                                         TISPKVORADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRIFTEAYV 120
                                                                                                                                                                                                                                                      DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                                                                                                                                                                    09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $9629;
01-MAY-2000 (TEBMBLrel. 13, Created)
01-MAY-2000 (TEBMBLrel. 13, Last sequence update)
01-MAX-2003 (TEBMBLrel. 23, Last annotation update)
Major capsid protein.
Sugar beet yellow virus (SBYV).
                                                                                                              1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKALVQKGAPNEGIEVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SNLSNLVITDASSLNGVDKKLLSAEVEMMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                   1 MELMSDDNLSGLVITDASSENGVDKKLLSAEVIKYLVQKGAPSGGIETVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKHKL PQLNAAAELGI PAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a plant virus.";
                                                         0;
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     Length 198;
                                                       indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perenysiov V.V., Hagiwara Y., Alzhanova D., Dolja V.V., Submitted (SEP-1999) to the EMBL/GenBank/DDBC databases. EMBL, AF190581; AAF1405.1; InterProv. IFR002679; Closter_coat. Pfam; PF03785; Closter_coat. SEQJENCE 204 AA; 22419 MW; FD6337E1D2490D33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20079557; PubMed=10611288; Peremyslov V.V., Hagiwara Y., Dolja V.V.; Hagiwara Y. Dolja V.V.; Hagiwara Y., Dolja V.V.; Hagiwara Y., Dolja V.V.; Proc. Oxfor Sci. U.S.A. 96:14771-14776(1999)
Query Match 92.9%; Score 921; DB 12;
Best Local Similarity 90.9%; Pred. No. 5.4e-82;
Matches 180; Conservative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VVNTPVSNLRCLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVNTPVSNIRÇLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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VTSLKQLGR 198
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Gaps

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7 SNLSNLVITDASSLNGVDKKLLSAEVEMMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                         29.8%; Score 295; DB 12; Length 204; 37.6%; Pred. No. 1e-20;
                                                                                                                   Indels
        22446 MW; D913184ECC93883B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. C1, Created)
01-NOV-1996 (TrEMBLrel. C1, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                   85;
                                                                                                                31; Mismatches
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                                                                                                                Conservative
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VTSLKQLGR 198
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                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Broom's barn;
        204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Z.)
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major coat protein.
Sugar beet yellow virus (SBYV).
Viruses; ssMx positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
WCBI_TAXID=12161;
                                                                                                                                    Coat protein (Fragment).
Sugar beet yellow virus (SBYV).
Viruses: ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                                                                                                                                                                             Creamer R., He X.H., Yang C.H., Grantham G.; "Characterization of the 3'-proximal encoded proteins of beet yellows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 YKHKLPQLNAAAELGIPAEDSYLAAJFIGTCPKLSELQQSRKMFASMYALKTEGGVVNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.9%; Score 296; DB 12; Length 204; 37.6%; Pred. No. 8e-21; ative 32; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Californian;
Dolja V., Peremyslov V., Hagivara Y.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBC databases.
EMBL, AFOS6575, AAC2512C1;
INCEPPC; IPR003679; Closter_coat.
Pfam: PF01785; Closter_coat.
Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   closterovirus.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 204 204 204 204 AA; 22419 MW; D082C33ECC93883B CRC64;
                                                   01-FEB-1997 (TrEMBirel. 02, Created)
01-FEB-1997 (TrEMBirel. 02, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
     204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, U71295; AAB17001.1; -.
InterPro, IPR002679; Closter_coat.
Pfam, PF01785; Closter_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.6%,
71; Conservative
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=California BYV-CA;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 VSNLROLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 VTSLKOLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=12161;
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SEQUENCE
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67 QRADSDVIFSNSFGE-RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                 126 YKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMPASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 QRADSJVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 YKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunstedt J., Moseley J., Hull R.;
"Nucleotide sequence of cDNA encoding the coat protein of beet yellows
                                                                                                                                                                                                                                                                                                                                                                                                                              Sugar beet yellow virus (SBYV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 SVQPTSTFIKASFGGGKELFLTHGELRSFLDSQKLLEGKPNKLRCFCRTFQKDYISFAKE
                           ? SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match 29.6%; Score 293; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 1.6e-20; Matches 71; Conservative 31; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
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90 KTPLVSAKIDAVNVIITYEDIKNFVNSLTLLKNYKNKLRVFARTFEBEYLRFVRÇYKHIL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 SDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYHHKL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 POLNAAAELGIPAEDSYLAAJFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTPVSNLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 PNIARANKHGIPADYSYLAADFVOTSNLLKEHEOA-VLLEGRNAATASSGTTRESAVNLK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 MNLHIDPIL -- IAMADVRQLGTQQNAALNRDL--FLTLKGKYPNLPDEDKDFHIAMMLYR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEXMLVQKG----APNEGIEVVFGLLLYA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LAARTIS--------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLXKVJD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Citrus tristeza virus.
Viruses: seRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                         "Characterization of the beet yellow stunt virus coat protein gene.";
Phytopathology 88:1040-1045(1998).
Bhytopathology 88:1040-1045(1998).
InterPro; IPR022049; Closter coat.
InterPro; IPR022048; EF-hand.
Pfam; PF01785; Closter coat.
SEQUENCE 215 AA; Z3696 MA; 91185835840806FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 NIVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 NFARASATCLNGENKKKLFEEFSVRVKTQDVTESGIPTTLGMTLYALATLSTSSKIDIED
                                                                             Lee R.F., Dawson W.O. yellow stunt virus
                                                                                                                                                                                          SEQUENCE FROM N.A.
Karasev A.V., Nikolaeva O.V., Lee R.F., Wisler G.C., Duffus J.E.
Dawson W.O.;
                             SEQUENCE FROM N.A.
MEDLINE=96266429, FubMed=8661428,
Karasev A.V., Nikolaeva O.V., Mushegian A.R., Lee R.F., Dawson Wersanization of the 3'-terminal half of beet yellow stunt virus genome and implications for the evolution of closteroviruses."; Virology 221:199-207(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.9%; Score 266.5; DB 12; Length 215; Best Local Similarity 36.1%; Pred. No. 6.7e-18; Matches 66; Conservative 22; Mismatches 94; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy A., Ramachandran P., Brlansky R.H.;
"Molecular characterization of Indian Citrus tristeza virus
isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match: 13.2%; Score 130.5; DB 12; Length.
Best Local Similarity 27.7%; Pred. No. 0.00014;
Matches 61; Conservative 27; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL/GenBank/DDBC databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXBL, AF501867; AAM22216.1; -.
InterPro; IPR002679; Closter_coat.
Pfam; PF01785; Closter_coat; 1.
SEQUENCE 223 AA; 24503 MW; 9D31F82AD158B649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update;
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Closterovirus.
NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 016 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 YLG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein.
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            NARARKERARKARAN OOOOOOO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 QRADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRIFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 NVQPTSTFIKASFGGGKELYLTHGELNSFLGSQKLLBGKPNKLRCFCRTFQKDYISLRKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTISPKV 66
                                                                                                                                                                                                                                                         Coat protein.
Sugar beet yellow virus (SBYV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %65858;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
Coat protein.
Beet yellow stunt virus.
Wiruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
NCBI_TAXID=35290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 YKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91116305; PubMed=1990061; MEDLINE=91116305; PubMed=1990061; Agranovsky A.A., Boyko V.P., Karasev A.V., Lunira N.A., Koonin E.V., Doblja V.V.; "Nucleotide sequence of the 3'-terminal half of beet yellows clostercvirus RNA genome: unique arrangement of eight virus genes."; J. Gen. Virol. 72:15-23(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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Lunina N.A., Atabekov J.G.;
Lunina N.A., Atabekov J.G.;
Lunina N.A., Atabekov J.G.;
Jenty Pilows Closterorius: complete genome structure and identification of a leader papain-like thiol protease.";
Virology 198:311-324(1994).
Virology 198:311-324(1994).
EMBL; X33465; CAA31564.1.
InterPro; IPR002679; Closter_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.9%; Score 286; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 7.7e-20; Matches 71; Conservative 29; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA; 22356 MW; 538E8E5811831486 CRC64;
                                                                                                                                                                                        01-NOV-1996 (TrEMBirel, C1, Created)
01-NOV-1996 (TrEMBirel, 01, Last sequence update)
01-MAR-2003 (TrEMBirel, 23, Last annotation update)
                                                                                                                                                 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-UKRAINIAN;
MEDLINE-94082464; PubMed-8259666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                       Q08531;
01-NCV-1996 (TrEMB1rel.
|::|:|:|:|
190 VTSLKQLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|:||:||
190 VTSLKQLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                             Closterovirus.
NCBI_TaxiD=1216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coat protein.
SEQUENCE 20
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11;

57; Gaps

065858

-1

Gaps

1;

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108 LRIFGRIFIEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLKKVLDGCAPLTRFTNK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 LRVWGRINDALYLAFC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL-TGAGLTDLECAVY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 LDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 IAMNDVRQLGTQQNAALNRDL--FLTLKGKYPNLPDKDKDFHLAMMLYRLAVKSSSLQSD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 LAARTISPKVORAD------SOLIF-SNSFGERNVVVTEGDLKKV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYA 56
       no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LVITDASSLNGVDKKLLSAEVEKMIVQKG----APNEGIEVVFGLILYALAARTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 MNLHIDPTL--IAMNDVRQLGTQQNAALNRDL--FLTLKGKYPNLPDKDKDFHIAMMLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATIN=TAW11;
STRAIN=TAW11;
Herrera-Isidron L., Villarreal-Garcia L.A., Rivera-Bustamante l'
Martinez-Soriano J.P.;
"Molecular Analysis of Citrus tristeza virus from Mexico.";
"Molecular Analysis of Citrus tristeza virus from Mexico.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF342890; AAK27476.1; -
InterPro; IPR002679; Closter coat.
InterPro; IPR002679; Closter coat.
Pfam; PF01785; Closter coat.
SEQUENCE 223 AA; 24868 MW; 6EAGC742D2212949 CRC64;
                                                                                                                                                                                                Martinez-Soriano J., Villarreal-Garcia J.A., Rivera-Bustamante Martinez-Soriano J.P.;
"Molecular Analysis of Citrus tristeza virus from Mexico.";
"Molecular Analysis of the EMBL/GenBank/DDBJ databases.
EMBL, AF342894, AAK27480.1;
-InterPro; IFR002679; Closter coat.
Pfam; PF0.785; Closter coat.
SEQUENCE 222 AA; 24741 MW; SBFA27BCB4B08DDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 LAVKSSS--LOSDDDTTGITYTREGVDVDLPDKLWTDVVFNSKGIGNR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.7%; Score 125.5; DB 12; Best Local Similarity 26.8%; Pred. No. 0.00044; Matches 56; Conservative 29; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match 12.7%; Score 125.5; DB 12; Best Local Similarity 27.0%; Pred. No. 0.00044; Matches 60; Conservative 27; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 MFASMYALKTEGG -- VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Citrus tristeza virus.
Viruses, ssRNA positive-strand viruses,
       Viruses; ssRNA positive-strand viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                           NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12162;
                                                                                                                                                                           STRAIN=BC15-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Closterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
       SOURTH PARK NOCCOSE THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 DDTTGITYTREGVEVDLSDKLWTDIVYNSKGIGNR------TNA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 LRTFGRIFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRX 167
   97 GCAPLTRFTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTC 156
                                                                                                                                                         133 -----TNALRVWGRINDALYLAFC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL-TG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 LRVWGRINDALYLAFC-RONRNLSYAGRPLDAGIPAGYHYLCADFL-TGAGLTDLECAVY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequeira Z., Nolasco G.; "Bacterial expressed cost protein for the development of a single antibody for routine detection of Cirrus Tristeza Virus in Portugal."; Submitted (SEP-1999) to the EMBL/GenBank/DBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 ITMNDVRQLSTQQNAALNRDL--FLALKGKYPNLPDKDKDFHIAVMLYRLAVKSSSLQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonacalza B., Febres V., Niblett C.L., Nolasco G.; "Blomolecular characterization of Citrus Tristeza Virus isolates from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LVITDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYALAARTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF184115; AAD56568.1; -... InterFror; IPR002679; Closter_coat. PF01708; Closter_coat. Ffam; PF01708; Closter_coat; 1. SEQUENCE 223 AA; 24930 MW; 05C456BD17C2D7F0 CRC64;
                                                                                                                                                                                                                                        157 PKLSELOOSRKMFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
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Best Local Similarity 26.3%; Pred. No. 0.00018;
Matches 55; Conservative 31; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 MFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 IQAKEQLLKKRGGDEVV---VTNVRQLGK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel: 13, Created: 01-MAY-2000 (TrEMBLrel: 13, Last seq 01-DEC-2001 (TrEMBLrel: 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0990P0;
01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-OCT-2001 (TrEMBLrel. 18, La
Coat protein.
Citrus tristeza virus.
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NCBI_TaxID=12162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 MNLHIDPTL--IAMNDVRQLGTCQNAALNRDL--FLTLKGKHPNLPDKDKDFHIAMMLYR 86
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STRAIN=19-21;
STRAIN=19-21;
Sequeira 2., North and the development of a single antibody for routine detection of Citrus Tristeza Virus in Portugal.";
Submitted (SPP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1841114, AMDS.657.1;
INTERPRO, IPR002679; Closter coat.
Pfam; PF01785; Closter coat.
SEQUENCE 223 AA; 24386 MW; 20723BBA-9E2CBFF CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 torprotein:
Citrus tristeza virus (isolate T38) (CTV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Gaps
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12.7%; Score 125.5; DB 12; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.00044;
Matches 60; Conservative 27; Mismatches 74; Indels 61;
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                                                                                155 TCPKLSELOQSRKMFASMYALKTEGG--VVNTPVSNLROLGR 194
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PRELIMINARY;
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01-DEC-2001 (TrEMBLrel.
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01-MAY-2000 (TrEMBLrel.
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Q8B3T3;
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Closterovirus. NCBI_TaxID=31712; [1]

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99 APLIRFINKERIFGRIFIBAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFEGTCPK 158
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SEQUENCE FROM N.A.
MEDLINE=99307427; PubMed=10377432;
Satyanarayana T. Gowda S., Boyko V.P., Albiach-Marti M.R.,
Mawasi M., Navas-Castillo J., Karasev A.V., Dolja V., Hilf M.E.,
Lewandowski D.J., Moreno P., Bar-Joseph M., Garnsey S.M., Dawson W.O.,
"An engineered closerovirus RNA replicon and analysis of heterologous
terminal sequences for replication.",
Proc. Natl. Acad. Sci. U.S.A. 96:7433-7438(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PNEGIEVVFGLLLYALA
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                                                                                                                                                                                                                                                                                                               Satyanarayana T., Gowda S., Ayilon W.A., Dawson W.C., "Frameshift mutations in infectious cDNA clones of Citrus tris virus. A strategy to minimize the toxicity of viral sequences Escherichia coli.".
Submitted (OCT-2002) to the EMBL/GenBark/DDBJ databases.
EMBL: AYI70468: AA012723.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%; Score 125; DB 12; Length 223; 25.9%; Pred. No. 0.00049; cive 33; Mismatches 63; Indels 64
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BJ37655 BJ37636

BJ37655 BJ37636

BG916284 QHB17G94,

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BG9831014 QGF27F14,

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BG9931014 QGF27F14,

BG982386 GGB16E23,

BF598403 SV17bC6, Y

BG77601, BG77601,

BG77608 GCG16C21,

BG77608 GCG16C21,

BG77608 GCG16C22,

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BQ986943.
BQ986943.1 GI:22404468
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BM132093 TGESTZyb0
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BZ434184 BONFR91TF
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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AZ691220 ENTJJ41TF
BI199349 602759615
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BU410316 603158538
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                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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EST 21-AUG-2002

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales, Brassicaceae, Brassica.

1 (bases 1 to 748)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
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jnr57h07.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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/note="Wetcor: pCYQN43; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica cleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Babinowicz (CSH1) and the shotgun library prepared at Washington University Genome
                                                                                                             -----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyr 126
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                                                                                                                                          ---- AlaAspPheleuGlyThrCysPro
                                                                                                                                                                                                                 127 LyskisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSer
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Mismatches:
Indels:
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Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: jnr57 row: h column: 07
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                         158 LysleuSerGluleuGlnGlnSerArgLysMet 168
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
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High quality sequence stop: 551.
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Cichorieae; Lactuca,

(Dases I to 706)

Kozik, A., Michelmore, R.W., Knapp, S., Marvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, C., Ellison, J., P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,

church, S., Jackson, L. and Bradford, K. of Chousitae Genome Project

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://ornggenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal 32
                                                                                                                                                                                                                                                                                                                                                                             Email: akozikatgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig GG_CA_Contig3108, see http://cgpdb.ucdavis.edu/
for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 GluiysMetLeuValGlniysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Ascumbson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742.1742
Fax: 1-(530)-752-9659
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for details.
Plate: QGF10 row: N column: 21.
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Hordeum vulgare subsp. vulgare
Elodeum vulgare subsp. vulgare
Elwaryota; Vicidiplantae; Srreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
The subtracted library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library Scource: David Sibley, Washington University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 TICTCCACGACCACCATIGCTTATIGTATICACAGTIGCTGTGGGGCTTCTTATGAAAAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LysLeuProGlnLeuAsnAlaAla.--AlaGluLeuGlyIleProAlaGluAspSerTyr 147
                                                                                                                                                                                                                                                                                                                                                             GluGlyAspLeuLysLys---ValLeuAspGlyCysAlaProLeuThrArgPheThrAsn 106
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/mol_type="mRNA"
/cultivar="barke"
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Institute of Plant Genetics and Crop Plant 1
Corrensstr. 3, 06466, Gatersleben, Germany
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EQ-PRIME, mRNA sequence.
EQ459495 GI:21267266
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1 (bases 1 to 562)
Radchuk, V., Zhang, H., Weschke, W.,
Barley ESTs from developing seeds
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/clone="HA08017"
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Insert Length: 562 Std Error:
Plate: 8 row: O column: 17
Seq primer: M13rev.
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Tel: 039482-5522
Fax: 039482-5595
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TgESTzybü6e07.y1 TgRH Tachyzoite Subtracted cDNA,Library Toxoplasma
gondii cDNA clone TgESTzybü6e07.y1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: toxo@waison.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40PF from Gibco
High quality sequence stop: 420.
Location/Qualifiers
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                                                                                                                                                                                                                                           141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                         551 ATAACCATCGTGGAAGGCACCTACGACAAATCTTAGGGAGTGATGGCCTGACGATGCTC 492
                                                                                                                                                               122 PheCysIleAlaTyrLys---HisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGly 140
                                                                                                                                                                                                    431 TTTGATCTCAAGGAAGGTCACAAGATTACAGGGTTCCATGGACGAGCTGGCGCGACT 372
                                                                                                                                                                                                                                                                                                                        161 GluieuglingInserArgiysMetPheAlaSerMetTyrAlaLeuiysThrGlugiyGly 180
                                                                                                                                                                                                                                                                                                                                                             320 CCTGCACAACCAACCAAGAAG----------CTAGAAGCTAAGGTGGT 282
      ValValValThrGluGlyAspLeuLysLysValLeu----AspGlyCysAlaProLeu 101
                                                                                  ThrargPheThrasnlysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAsp 121
                                                                                                                                                                                                                                                                  Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108, USA
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxoplasma gondii
Toxoplasma gondii
Bukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Excocystidae; Toxoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 CTTGGGAGGAACGCAGGTTAGATGCAGTCGAGTTGTTTGATAGGATGTGCAAAGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 CysalaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LysHisLys 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 GIGGAIGACGCIGITGGITACTICAGCAAGAIGITIGATGITGGICTCAGGCCCCAAIGC 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 CCIGACGAATACACTTATGTCTTA-----CTCATTGAGTCCTGCTTCAGGGTTGATAAT
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/dev_stage="0-7 DAP (days after pollination)
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Lactuca sativa

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.

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Cichorianta, Nichelmore, R.W., Knapp, S., Marvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., J., Kohman, J., Slabaudh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower Ests from the Compositae Genome Project

Http://compgenomics.ucdavis.edu/
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/ clone lib="QG FEGH/ lettuce serticla"

/ construction can be obtained at http://cgpdb.ucdavis.edu/

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Department of Vegetable Crops, R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
Norbersity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Fax: 1-(530)-752-9659
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 704)
Town, C.D., Van Aken, S., Jtterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
Unpublished
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                                                                                  55 TTAGATTTGACAGCAAAGAGTGGTATTAATGTTGTACATTGTCCAGAATCAAATTTAAAG 496
                                                                                                                                                                                                                ------ThrAsnLysLeuArgThrPheGlyArgThrPheThr 116
                                                                                                                                                                                                                                                                                                  117 GlualaTyrValAspPheCysIleAlaTyrLysHisLysLeuPrcGlnLeuAsnAlaAla 136
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603 TCATCATCATTGATTGCAGCTCATATGACA------CAATTAACAAGTGAAGAT 556
                                          ValilePheSerAsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLys
                                                                                                                             93 LysValLeuAspGlyCysAlaProLeuThrArgPhe------------
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total_bNA inserted_into_pH0S1 using_BstXI_linkers"
168 c 144 g 223 t
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BONFR91"
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Brassica oleracea
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Fax: 301-838-0208
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                                                                ------ CCTGGTGGACTT--- 411
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                      ------AsmSerPheGlyGluArgAsnValValValThrGluGlyAspleuLys 92
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/clone_lib="Dictyostelium discoideum cDNA library, VF"
129 c 96 g 227 t
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Dictyostelium discoideum
Eukaryota, Myoctoza, Dictyosteliida, Dictyostelium.
1 (Dases 1 to 671)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 bp mRNA linear BJ433495 Dictyostellum discoldeum cDNA library, VN discoldeum cDNA clone ddv22f05 3', mRNA sequence. BJ433495. GI:19408217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
11:11 Yara, Mishima, Shizuoka 4:1-8540, Japan
Fal: 91-559-81-6856
Fax: 31-559-81-6855
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Location/Qualifiers
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Eukaryota; Mycetozca; Dictyosteliida; Dictyostelium.
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                    74 TCTGACCTCAACAACAAGTACATGCAACTTGCCTCTCAATCTCAAGGCTTTGGAGAGTCAA 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CATCATCATTGATTGCAGCTCATATGACA-------CAATTAACAAGTGAAGAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
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                                                                                     Institute of Biological Sciences
University of Taukuba
1-1. Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Tex: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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(6), 335-340 (1998)
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                  Contact: Hideko Urushihara
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/doing libe "OH ABCDI sunflower RHA801"
/doong libe "OH ABCDI sunflower RHA801"
/dote="Vector: pBBcDNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QH_ABCDI sunflower RHA801
TAG_LIB=QH_ABCDI sunflower RHA801
TAG_LISUE=Shoots environmental stress
110 c 175 g 168 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asteridis campanulids. Asterales, Asteraceae, Asteroideae; Helianthus.

1 (Dases I to 634)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elliscn, P., Kolkman, C., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K., Chou, Y., Lai, Z., Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                             169 PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188
333 ---GAAGGTGGTGAACCTGTAACACCATCATATAAGATTTTGTCAATGGCAACTATTAAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Fax: 1-(530)-752-9659
Fax: akozik@argc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                             654 bp mRNA linear EST 19-AUG-20
QHB17G04.yg.abl QH ABCDI sunflower RHA801 Helianthus annuus cDNA
Clone QHB17G04, mRNA sequence.
                                          149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysMet
                                                                                    276 GGTGCAAAGGCATTGGGTATCGATGATAAGTTGGTTCACTTCAAATTGGTAAA----
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Helianthus annuus
                                                                                                                                                                                                                        189 LeuArgGlnLeuGlyArgArgGluVal 197
                                                                                                                                                                                                                                                                  162 TTAGTTTAGGTACTAATCATGTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 TTAGATTTGACAGCAAAGAGTGGTATTAATGTTGTACATTGTCCAGAATCAAATTTAAAG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ThrAsnLysLeuArgThrPheGlyArgThrPheThr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GluAlaTyrValAspPheCysLleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LeuLeuTyralaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAsp 72
                                                               linear EST 08-MAK-z.
cary, CF Dictyostelium
                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 751)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="mat A"
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| 139 c 104 g 264 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 GTTGGTACTGATTCTGCCGCTAGTAATGATTTAGATATGTTGGGTGAATTACGTACT
                                                          BJ376355
BJ376355 Dictyostelium discoideum cDNA library, C discoideum cDNA clone ddc28n02 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
Location/Qualifiers
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/ mol_type="mRNA"
/ strafin="AAA" / 44689"
/ clone="ddc28n02"
                                                                                                                                                                                                                                                                                                                                                                    Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-854C, Japan
Fax: 81-559-81-6855
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BJ376355.1 GI:19285738
EST
Dictyostelium discoideum
Dictyostelium discoideum
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ed. No.:
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AUTHORS
TITLE
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Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozikāatgc.org (michelmore@vegmail.ucdavis.edu) belongs to contig QG_CA_Contig3108, see http://cgpdb.ucdavis.edu/ for details.	BASE COUNT 157 a 104 c 175 g 174 t CRIGIN Alignment Scores:	53 LeuLeuTyralaLeuAlaAlaArgThrThrSerProbabilities 53 LeuLeuTyralaLeuAlaAlaArgThrThrSerProbabilities 54
### Conservative: 31 ### State	103 ArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGlualaTyrValAspPhe 122 133 Cys:leAlaTyrLySHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyllePro 142 153 Cys:leAlaTyrLySHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyllePro 142 153 TTGAGACGGATCAGGAAAAACACTTTTGTTGGTGTTCTTGATTCT 352 143 AlaGluAspSerTyzLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160 111	SULT 11 84646 B0848646 B0848646 CUS FINITION GGATMO1.yg.abi GG_ABCDI lettuce salinas Lactuca sativa cDNA clone GGATMO1.yg.abi GG_ABCDI lettuce salinas Lactuca sativa GGATMO1.yg.abi GG_ABCDI lettuce salinas Lactuca sativa GGATMO1.mRNA sequence. GESSION B0848646.1 GI:22234115 BCSION BO848646.1 GI:22234115 BCSION BORGANISM BCSION BCSIO

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GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu 52
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/tissue_type="leaf"
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TITLE
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// Jab hose Sericoli"
// Cone lib="GG EFGHL lettuce serricola"
// Cone lib="GG EFGHL lettuce serricola"
// Cone lib="GG EFGHL lettuce serricola"
// Cone service sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distribuish each
source of RNA. CDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
cransformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_INSUB_CHemical induction
TAG_INSUB_CHemical induction
TAG_INSTANCECHEMICAL
TAG_SEQ_INSTANCECHEMICAL
TAG_SEQ_INSTANCECHEMICAL
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TAG_SEQ_INSTANCECHEMICAL
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TAG_
                                                                                                                                           mRNA linear EST 21-AUG-2062 serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 611)

Koaix, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Koaix, A., Michelmore, R.W., Lavelle, D., Chevaller, P., Ziegle, J.,
Elison, P., Kolkman, J., Slabaudh, M.S., Livingston, K., Zhou, Y., Eai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
Unpublished
                                                                                                                                                                                                                                                                                                               Lactuca sativa
Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Assuradson Hall, UCD, Davis, CA 95616, USA
7el: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgg.org [michelmore@vegmail.ucdavis.edu;
belongs to contig QG_CA_Contig3108, see http://cgpdb.ucdavis.edu/
for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 VallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal 32
611
23
47
59
13
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
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Matches:
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                                                                                                                                     GGESAOS. yg.abl QG_EFGHJ lettuce QGESAOS, mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGE5A65"
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BG526441 632 bp mRNA linear EST 16-NOV-2001 61-95 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
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/lab_host="E. coli strain XLOLR"
/clone lib="Stevia field grown leaf cDNA"
/note="Vector: pBK-CMV, Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed_from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 -----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 LysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGiyIleProAlaGluAspSer 146
                                                                                                                            263 GTTGAAGTTGTGACGCCTGAAGAACATTTGGGGGATGTGATTTGGGGATTTTGAATTCGAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AGAGGCCACATTAATAGCTTTGGTGATAAG-------CCTGGTGGACTT--- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LysvalLeuAspGlyCysAlaProLeuThr-----ArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AAGGTGGTGGATTCTTTGGTCCCACTTGCGGAAATGTTTCAGTATGTGAGTACTTTAAGG 424
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1 (bases 1 to 632)

Brandle,J.E., Richman,A., Swarson,A.K. and Chapman,B.P.
Leaf ESTs from Stevia rebaudiana: A resource for gene discovery diterpene synthesis
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 ------TyrLeuAla-----AlaAspPheLeuGlyThrCys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 TCTTCATCTTTGTGCTATTAATGATAGGGGAATTTTCTGATTTTCACTTCATATGT 601
                                                                              LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys-----ValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                 ------AsnSerPheGlyGluArgAsnValValThrGluGiyAspLeuLys
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Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC
1391 Sandford St., London, Ontario, CANADA, NSV 4T3
Tel: 519 457 1470
Fax: 519 457 1397
Email: brandleje@em.agr.ca
Seq primer: T3 promoter primer.
Location/Qualifiers
191 -----creccaccaccaccartrcccaaacart
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asterids; campanulids; Asterales; Asteraceae; Asteroideae;
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DB:
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ORIGIN
                                                             AUTHORS
                                           REFERENCE
                                                                                                                JOURNAL
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                                                                                                                                COMMENT
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were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The CDNA was prepared using an Xhol-poly(dT) linker-primer. An EcoRI adapter was lighted to the blunt end cDNA and the products were digested with EcoRI and Xhol enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the bost strain XLI-Blue MRF' Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOLR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTACTAAAAGGGA 3' This library was constlucted by Alex Alchman." I others
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leaf cDNA Stevia rebaudiana cDNA 5', mRNA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 ------AGGAAAGCGGGTCCCAAGATTTGGAACCCATATGAGAGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ThrPheG'yArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHis
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Stevia rebaudiana
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BG523153.1
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st Local Similarity:
ery Match:
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YWCRDS
URCE
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Bupatorieae, Stevia.

Supatorieae, Stevia.

Stevia.

Stevia.

Stevia.

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Stevia.

Stevia.

Stevia.

Stevia.

Subandie, Ja.

Subandie, Ja.

Subandie, Ja.

Subandie, Ja.

Subandie, Subandie

Genomics and Biotechnology

Agriculture and Agri-Food Canada - SCPFRC

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1 (bases 1 to 695)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M.; Rieseberg, J.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichcrioideae;
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Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig3108, see http://cgpdb.ucdavis.edu/
----AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysVal
                                                                                                                                                   95 LeuAspGiyCysAlaProLeuThr-----ArgPheThrAsnLysLeuArg-----
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University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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/cultivar="L.serriola"
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